

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_p2n model

Run on: January 21, 2006, 07:52:59 ; Search time 396 Seconds

(without alignments)  
2797.533 Million cell updates/sec

Title: US-10-066-521-6

Perfect score: 7074  
Sequence: 1 MEGAKSLTFFSYGLQMCLEYE.....DDHSGVSWSLGAGLGLVLS 1344

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 6049916 seqs, 412136615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-Model=frame+ p2n.model -DEV=xlh  
-O=/cgn2/1/USPRO/epool/US1006521/runat 20012006.145900.21124/app.query.fasta.1.1543  
-DB=Published Applications NA New -QFMT=fastap -SUFPRX=p2n.rmpbn -MINMATCH=0.1  
-LOOEXT=0 -LOOEXT=0 -UNITS=bits -STRAT=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US1006521.@CEN 1.1.277.@runat 20012006.145900.21124  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New.\*

1:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
2:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
5:	/cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
6:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.1*
8:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
9:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.2*
10:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.3*
11:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1248.5	17.6	3189	8	US-11-137-465-10
2	1217	17.2	3150	8	US-11-137-465-9
3	957	13.5	5100	8	US-11-136-527-4000
4	364	5.1	4390	8	US-11-136-527-4006
5	359.5	5.1	3382	7	US-10-966-846-1
6	347	4.9	2859	7	US-10-966-846-3
7	280	4.0	3213	8	US-11-147-047-23

8	276	3.9	3072	8	US-11-145-631-3	Sequence 3, Appl1
9	276	3.9	3133	8	US-11-136-527-4003	Sequence 4003, Ap
10	276	3.9	3133	8	US-11-145-631-1	Sequence 1, Appl1
11	276	3.9	3612	8	US-11-145-631-6	Sequence 6, Appl1
12	276	3.9	3615	8	US-11-145-631-4	Sequence 4, Appl1
13	276	3.9	3615	8	US-11-145-631-12	Sequence 12, Appl
14	270	3.8	536	8	US-11-128-061-276	Sequence 276, App
15	270	3.8	536	8	US-11-128-061-3918	Sequence 3918, Ap
16	270	3.8	536	8	US-11-128-049-276	Sequence 276, App
17	270	3.8	536	8	US-11-128-049-3918	Sequence 3918, Ap
18	169.5	2.4	1068	7	US-10-750-185-27825	Sequence 27825, A
19	169.5	2.4	1068	7	US-10-750-623-27825	Sequence 27825, A
20	168.5	2.4	1068	7	US-10-750-623-27825	Sequence 22, Appl
21	166	2.3	1925	7	US-10-750-185-55918	Sequence 55918, A
22	166	2.3	1925	7	US-10-750-623-55918	Sequence 55918, A
23	151	2.1	1400	8	US-11-136-527-8099	Sequence 8099, Ap
24	149	2.1	2148	8	US-11-136-527-8099	Sequence 1594, Ap
25	149	2.1	2148	8	US-11-136-527-8099	Sequence 28, Appl
26	146.5	2.1	2144	7	US-10-624-932-15	Sequence 15, Appl
27	145.5	2.1	2187	7	US-10-624-932-17	Sequence 17, Appl
28	143	2.0	6111	8	US-11-136-527-3837	Sequence 3837, Ap
29	143	2.0	5984	8	US-11-091-928-3	Sequence 3, Appl1
30	138.5	2.0	5366	8	US-11-091-928-3	Sequence 4, Appl1
31	136.5	1.9	3573	8	US-11-136-527-4096	Sequence 4096, Ap
32	135.5	1.9	1681	7	US-10-632-150-53	Sequence 53, Appl
33	135.5	1.9	1681	8	US-11-073-457-53	Sequence 53, Appl
34	135.5	1.9	1681	8	US-11-073-457-53	Sequence 53, Appl
35	135.5	1.9	6269	8	US-11-136-527-2572	Sequence 2572, Ap
36	134	1.9	9136	8	US-11-136-527-2808	Sequence 3808, Ap
37	133.5	1.9	4059	7	US-10-632-150-47	Sequence 47, Appl
38	133.5	1.9	4059	8	US-11-073-457-47	Sequence 47, Appl
39	133.5	1.9	4059	8	US-11-073-457-47	Sequence 47, Appl
40	132.5	1.9	1320	7	US-10-750-185-60781	Sequence 60781, A
41	132.5	1.9	1320	7	US-10-750-185-60781	Sequence 60781, A
42	132.5	1.9	7474	8	US-11-069-834-49	Sequence 49, Appl
43	132	1.9	3132	7	US-10-821-234-224	Sequence 224, App
44	130.5	1.8	33018	8	US-11-077-716-1	Sequence 1, Appl1
45	129.5	1.8	116856	8	US-11-143-980-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-11-137-465-10  
Sequence 10, Application US/11137465  
Publication No. US2005025558A1  
GENERAL INFORMATION:  
APPLICANT: Agarwal, Pankaj  
APPLICANT: Murdoch, Paul R.  
APPLICANT: Rizvi, Safia, K.  
APPLICANT: Smith, Randall, F.  
APPLICANT: Xiang, Zhaoqing  
APPLICANT: Kahlback, Karen  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: GPO50018  
CURRENT APPLICATION NUMBER: US/11/137,465  
CURRENT FILING DATE: 2005-05-25  
PRIOR APPLICATION NUMBER: US/10/239,663  
PRIOR FILING DATE: 2002-09-24  
PRIOR APPLICATION NUMBER: PCT/US01/09226  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 60/192,158  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: 60/192,668  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: 60/200,166  
PRIOR FILING DATE: 2000-04-27  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 3189  
TYPE: DNA  
ORGANISM: Homo sapiens

## US-11-137-465-10

## Alignment Scores:

Pred. No.:	1.15e-105	Length:	3189
Score:	1248.50	Matches:	335
Percent Similarity:	47.17%	Conservative:	199
Best Local Similarity:	29.59%	Mismatches:	459
Query Match:	17.65%	Indels:	139
	8	Gaps:	23

US-10-066-521-6 (1-1344) x US-11-137-465-10 (1-3189)

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Qy 12 TyrglyleuglntrpCysleuTyrglyleuaplysuglnupheglnthrpheylsglu 31
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 25 TTCACCTGACGAGCTCTCTGAGCAGCTCAGCAGATGATGAGCAATTGACAGAT 84
Qy 32 LeuleuylslylserserGluserThrCysSerllleProgluphegluilegu 51
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 85 CTGATCAGACCTTCTCTGAGCAGCAGAGCTCCAGAGATCCCCACAGAGAGTGAAC 144
Qy 52 AsnAlaasnValglucylsleuAlaleuileuHnlsgluTyrrglAlaSerleuAla 71
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 145 AAGCTGATGGAGGACCACTGTAGAAATCTTACACACCTGATGACAGCTACTGGGTG 204
Qy 72 TrpAlaThrSerllleSerlllePhegluabmetasnuEuargThrLeuSerGlulysAla 91
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 205 GAGATGGCAGACCTCCAGGCTTTGAAAAGATGACCGAATGATCTGTGTGAGAGAGCA 264
Qy 92 ArgAspAspMetlylsylleSerGlAlaMetgluIngu----- 105
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 265 AAGCATGATGACAGAGAGCAGCTTGTGAAATCTTTATATAAGAGACCTTATCATTA 324
Qy 106 GlValaThrAlaAlagluThrgluInguInuIleSerGlAlaMetgluInguIngu 125
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 325 GGGATTAACAAGGAAACGACCACTTACAGCTGAGACGAATGCTGAGCGCTTCAAA 384
Qy 126 AlaThrAla--AlagluThrgluInguInuHnls-----GlyGlyAspThr 140
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 385 ACAGAGACAGAAAGCTTTACAGAAACGAAGAATGATCATGCTGCGTGAAGAAAGTC 444
Qy 141 TrpAspTyrrlysSerHnls-----ValMetThrLysPhe 151
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 445 TTTTAAAGAAAAGAAAGCCAGACAAAGATAGTGACAGTATATATGAAACAGAAAGTTC 504
Qy 152 AlaGlugluInuAspValArgArgSerPhegluabnThraAlaAspTrpProgluMet 171
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 505 -----CGGAGATGTGAGAGAGCTGGCTGAGATGAGAAAGAGTTC 546
Qy 172 GlInThrleuAlaglyAlaPheAspSerAspArgTrpGlyPheArgProArg----- 188
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 547 CAGGTATAGCTGAGATCAAGATGATGCCATTCAGCAACCCAGAGGTGCTTCCC 606
Qy 189 -----ThraValleuHnlsGlyLysSerGlylleGlyLysSerAlaLeu 203
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 607 GGGCCCTTTCATACACGCTGTGTCTGTATGTCTCTGACGAGCTTGGGAAAACACAGCTG 666
Qy 204 AlaArgArglleValleuCysTrpAlaGlInglYglYleuTyrrglInuMetPheSerTyrr 223
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 667 GCCCAAGAACTTAAGCTAGACTAGGAGGAGCAACCTCATTCAC--AAATTCAAATAT 723
Qy 224 ValPhePheleuProValArgGlumetClnArglylsylgluSerSerValThrGluPhe 243
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Db 724 GCGTTTACCTCAGCTGAGGAGAGCTCAGCCGCTGGGCGCGTGCAGATTGGCAGAGTGG 783
Qy 244 lleserArgluTrpProAspSerGlAlaProValThrgluIleMetSerArgProglu 263
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 784 GTCTTACAGGAGCTGCTGAGATTCAGAGATGACATTCACATCTCTAGCCAGACAGCG 843
Qy 264 ArgleuLeuPheIlelleAspGlyPheAspAspLeuGlySer-----ValleuAsn 280
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 844 AAAATCTTGTTCGTGATTTGACGCTTTGATGAGCTGGAGCCGACCTGGGGCGCTGATC 903
Qy 281 AsnAspThrLysleuCysLysAspTrpAlaGlulysgluInProPheThrleuIleArg 300

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Db 904 GAGAGC-----ATCTCGGAGACTGGAGAGAAAGACCGGTGCGCTCTCTGAGG 957
Qy 301 SerleuLeuArgylsValleuLeuProgluSerPheleuIleValThraValAspVal 320
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 958 AGTTTGTGAACAGGAGTGAATTTTCCAAAGCGCGCTGTGTGTACACAGCGGCCAGG 1017
Qy 321 GlYThrGlulysleuLysSerGlulValSerProArgTyrrleuLeuValArgGlylle 340
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1018 GCCCTGAGGAGACCTCCGAGTCTGCGGAGAGAGCCGATCTACATTAAGGTGAGAGGCTTC 1077
Qy 341 SerGlygluInuArglleHnlsleuLeuGlulnArglylleGlylnHnlsGlnLysThr 360
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1078 CTGAGAGAGAGACAGAGAGGCGCTATTCTTGACACATTTGGAGACAGAGCAAGCATG 1137
Qy 361 GlInglYleuArgAlaIleMetAsnAspArgGlnleuLeuAspGlnCysgluInuAlaProAla 380
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1138 CGTGCTTTGAGCTTAAGAGAGACAGAGCGGCTGTTCAGCTGGGCTGAGCGCGCG 1197
Qy 381 ValGlySerleuIleCysValAlaleuGlnleuGlnAspValValGlygluSerValAla 400
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1198 GTGTGCTGATCGTGTGACAGACTGTGACAGTGTGAGAGAGGAGGAGACCGGTC 1257
Qy 401 ProPheAsnGlnThrleuThrglyleuHnlsAlaAlaPheValPheHnlsGlnLeuThrPro 420
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1258 CCCACCTGCTCCTACCCGACGAGGCTGTCTGCTGCTCTGTCAGACCGGTTG---CCG 1314
Qy 421 ArgGlyValValArgArgCysleuAsnleuGlnluInuArgValValleuLysArgPheCys 440
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1315 CAGGGCGCA-----CAGCTGGGAGGCGGCTGCGGACGCTGAGC 1353
Qy 441 ArgMetAlaValgluGlyValTrpAsnArgLysSerValPheAspGlyAspAspLeuMet 460
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1354 CTCTGGCCCGGACGAGGCGCTGTGGGCCGACAGACTCGTGTCTTACCGAGAGATCTGGA 1413
Qy 461 ValGlnGlyleuGlylsylgluSerGlyleuArgAlaleuPheHnlsMetAsnIleleuLeuPro 480
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1414 AGGCTCGGAGTGCAGAGATCCGACCTCGTGTCTCTGACGAGAGACATCTCCGCGAG 1473
Qy 481 AspSerHnlsCysgluInuTyrrThrPhePheHnlsleuSerleuGlnAspPheCysAla 500
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1474 GACAGACTCTCCAAAGGCTGTACTCTTATCCATCCACTGACCTTCCAGAGTTTCTACT 1553
Qy 501 AlaLeuTyrrValleuGlnGlyleuGlu----- 510
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1534 GCCCTGTCTACACCTCGAGAGAGAGAGAGAGAGATAGAGAGCGCCACACTGGAGAC 1593
Qy 511 -----llegluProAlaleuCysProleuTyrrValGlnuTyrrLysArgSerMet 527
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1594 ATTGGGAGCGTACAGAGACTGCTTTCCGGA-----GTAGAAAGATC--AGGAGACCC 1644
Qy 528 GluleuLysgluInuAlaglyPheHnlsIleHnlsSerleuTrpMetLysAspPheLeuPheGly 547
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1645 GACCTGATCCAGAGAGGCTAC-----TACTCTTTGGC 1677
Qy 548 LeuValSerGlunAspValArgArgProleuGlnuValleuLeuGlyCysProValProleu 567
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1678 CTGCGTACAGAGAGAGAGAGAGAGAGTGGAGGCCACTTTGGCTCCCGGATTCACCG 1737
Qy 568 GlYVallylsylgluLysleuLeuHnlsTrp--ValSerleuLeuGlylnuProAsnAla 586
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1738 GACATCAAGAGAAATGTGCGATGCGACATAGATTGAAGGTGACATTCAACGGTGG 1797
Qy 587 ThrThrProgluAspThrleuAspAlaPheHnlsGlyleuPhegluThrglnuAspGly 606
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1798 ACA-----GACCTGACAGAGCTCTCGGCTGTGTGACAGTGTCCAGAGAGAGAG 1848
Qy 607 PheValArgleuAlaleuAsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeu 626
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1849 CTGAGTGAAGAGAGTGAAGGCTCACTTCAAGAAATATCCCTGACCTTAATGCA--GTA 1905
Qy 627 AspLeuIleAlaSerSerPheCysleuGlnHnlsCysProTyrrleuAspGlylleArgVal 646
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Db 1906 GACGTGTGGCATCTTCATCTGGCGTCAGACAGCTGCGAAGCTGCAAGAAATGTCAGT 1965
Qy 647 Aspyal---lysglylepheroargapyluserialaglyalaCysProvalPro 665
Db 1966 CAGGTAAATAAGAGAAATCTCCGAGAAATGTCACCTGGCTGTAATCAGACCGCAGGTT 2025
Qy 666 LeutrpmetcagaplyrThreullegluclugluluarPheCysSermetreu 685
Db 2026 GAGAGATCCCAAGATGATCAGACACATGCTTCCTTGTGAGAGACCTTGTTCATATT 2085
Qy 686 GlyThrihProhVleuarggluleuapleuuglyserSerileuThrgluargla 705
Db 2086 GGATCAAAATAAGATCTGATGGGTCTAGCAATCAATGATAGCTTTCTGAGCCTCCCTA 2145
Qy 706 MetlystrleuCyvalalyleuarghIProthrcylyslleglThleumethe 725
Db 2146 GTAGAGATCTGTGTGAAACAAATAGCTCTGACACCTGTATCTCCAGAGAGTGTGTTTC 2205
Qy 726 ArgamlaaglInlethProglValaglInleuThraparglleValMetAlaenarg 745
Db 2206 AAAAATATTTCCCAAGCTGATGCTATGGAACCTTCTGCTAGCTCTTCAAGTCAAG 2265
Qy 746 AsnleuargSerleuAsnleuGlyglYThrihVleuylsgluuAspValArgmetAla 765
Db 2266 ACTGTAAAGTATCTGACCTTCAAGGCAAT-----GACCAAGATGATATTTCGCCCA 2319
Qy 766 ---CysglualaleuylVhIProlyrCysleuLeuuglyserleuargleuaprcys 784
Db 2320 TTGTGTGAGTCTTGAGACATCCAGAAATGTAACCTGCAATATCTCGGGTGTGTCTGT 2379
Qy 785 GlyleuThrihVlaIcyetrleuylleuSerInleuThreProserleu 804
Db 2380 TCCCGTACCTCAGACAGTGGCTGATCTCTCTTGGCCCTTGAAGTCAACAGCTCCCTG 2439
Qy 805 LyserleuSerleuAlaglVAsnlyValThrapargInglValMetProleuSerap 824
Db 2440 ACGTGAAGTAACTCCGCAAAATAGCTTGGATGAGGGGTGAAGTGTCTGATACACA 2499
Qy 825 AlaIeudargValserglInCysAlaleuclInlyleuileuugluarCysglYlethr 844
Db 2500 ACTTGAACACCCCAAGTGTCTTGTGCAAGGTGTGTGTGAAACTGTCACTTCA 2559
Qy 845 AlaThrglyCysglInSerleuAlaSerAlaSerAlaSerAlaSerleu 864
Db 2560 GAAGCAATTTGCAAGACCTTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2619
Qy 865 CysleuSerleuAsnSerleuGlyVanglulglValAsnleuLeuCyargSermetarg 884
Db 2620 TGCCTTGGCCAGAAACCCCATTTGGAAATACAGGGGTGAAGTTTCTGTGTAGGGCTTGAAG 2679
Qy 885 LeuProhIscYsserleuclInargleuMetleuAanglInCysVhIleuapThralaglY 904
Db 2680 TACCCCGAGTGAACCTGACAGACCTTGGCTTGAACCTGCAATGACATGACATGACAT 2739
Qy 905 CysglYPhelaleuAlaleuAlaleuMetglYAsnSerleuThrihIleuSerleuSer 924
Db 2740 TGCCTCGATCTTCAAAAGCTTCTTCAAGAAATAGTAAAGCTGTGTGTGTGTGTGTGTGTGT 2799
Qy 925 MetAnProvalgluAspAnglYValIyVleuLeuCygluValMetarggluProser 944
Db 2800 CTGAATCAGATAGAGATTAAAGGATGAAGTTCTCTGTGTGAGGCTTGTGAGAAACCACTG 2859
Qy 945 CysVhIleuclInapleuclInleuValIyCysVhIleuThralAlaCysCysgluSer 964
Db 2860 TGCACACTTG-----AGATGT----- 2874
Qy 965 LeuSerCyvalIleSerargSerarghIleuYsserleuapleuThrapamla 984
Db 2874 ----- 2874
Qy 985 leuGlYAspGlyglYValAlaIaleuCygluclYleuYglInlyAsnSerValleu 1004
Db 2874 ----- 2874

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Qy 1005 ThrapgluclYleuYAlaCysglYleuThreSerapCysCygluAlaleuSerleu 1024
Db 2875 -----CTGTGTGTGTGTGGATGTTTCATCTCCCGTTCATTTGTGAAGACTGTGCTCT 2928
Qy 1025 AlaLeuSerCyvalAnarghIleuThrSerleuAsnleuValglInAsnPheserPro 1044
Db 2929 GCCCTCAGCTCAACCAAGAGCTGTGCTGTGACCTGGGTCAAGATCCCTTGGGCTCT 2988
Qy 1045 LyseglMetmetlyVleuCySerAlaPhelAlaCysProthreSerAnleuclInlele 1064
Db 2989 AGTGAAGTGAAGATGCTGTGTGAACCTTGACATGTTCACATGGACCTTCGGAGACTC 3048
Qy 1065 GlyleuTrplyrTrpglInProvalglInlearglyVleuLeuclIngluValglInleu 1084
Db 3049 AGTTGAAATACGATGACTTAAATGATGATCAATGATAGCTGTGAGAAATAGAAAGA 3108
Qy 1085 LeuYsProargValIleAspGlyserTrphis 1096
Db 3109 AAAAACCAACTGATATTGATGATGAGAAACT 3144

RESULT 2
US-11-137-465-9
; Sequence 9, Application US/11137465
; Publication No. US2005025558A1
GENERAL INFORMATION:
; APPLICANT: Agatwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPE50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/US01/09226
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,158
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/200,166
PRIOR FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 3150
TYPE: DNA
ORGANISM: Homo sapiens
US-11-137-465-9

Alignment Scores:
Pred. No.: 1,01e-102 Length: 3150
Score: 1217.00 Matches: 333
Percent Similarity: 47.88% Conservative: 187
Best Local Similarity: 30.66% Mismatches: 470
Query Match: 17.20% Indels: 96
DB: 8 Gaps: 22

US-10-066-521-6 (1-1344) x US-11-137-465-9 (1-3150)
Qy 8 ThrpheSerTrpYglYleuclInTrpCysleuYr-----Gluleuaplyys 23
Db 76 ACTATGACATCGCCCAAGCTGAGTGAAGTCTGACAGACCTTCTGAGACAGCTGAACGAG 135
Qy 24 GluclInPhelInThrPhlygluleuLeuYslysserSercluserThrtrCys 43
Db 136 GATGAATTAAGAGATTAAATCCCTTTTATGGGCTTTTCCCTGGAAGAGCTGTACAG 195
Qy 44 SerleProglInPhelInleclInAsnValgluYsleuAlaleuLeuLeuThIs 63

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Db 196 AAGACCCATGCTGATGAGGAGAGCTGATGCAAGAACTGGCAGAAATTCCTGTC 255
Qy 64 GlnTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGluAenMetAen 83
Db 256 AAGACCTCTCCAGAAAATTGGATTAAGGAATGCCACTGTGAACATCTTGAAGAGATTAAT 315
Qy 84 LeuArgThrLeuSerGluTyrAlaArgAspAspMetLeuTyrIleSerGlnAlaMetGlu 103
Db 316 CTCACGGAATTTGTGAATGAGCAAGCTGAAAGTGAATGATGAGACGGAACGGTGCAGAA 375
Qy 104 GlnGluGlyAlaThrAlaAlaGluThrGluGlu---GlnGluIleSerGlnAlaMetGlu 122
Db 376 ATGATATATCTGAGCTGGAGATGACAGAAAGACTCGAGATTAGCAAGACCACTTTGG 435
Qy 123 GlnGluGly---AlaThrAlaAlaGluThrGluGluGlnGlnIleSerGlyAspThrTyr 141
Db 436 AAGGAGAGATGAGAAATTCATATGAGAAACAGCTTTGTGTGGAAGAACACCTTTTGG 495
Qy 142 AspTyrTyrSerHisValMetThrLeuPheAlaGluGluAerValAlaArgSer--- 160
Db 496 CAAGGAGAC-----ATTGACAAATTCATATGACACGCTGACCTGAGAAACCAACGG 546
Qy 161 -----PheGluAenThrAlaAlaAspTyrProGluMetGlnThrLeuAlaGlyAla 177
Db 547 TTCATTCATTCCTTGAATCCAGAAC-----CCAGAGAACTPAACA----- 588
Qy 178 PheAspSerAspArgTyrGlyPheArgProArgThrTyrAlaValLeuHisGlyLeuSerGly 197
Db 589 -----CCTTACACGGTGTGTGCTGCACGGCCCGCCAGGC 621
Qy 198 IleGlyLeuSerAlaLeuAlaArgArgIleValLeuGlyTyrTrpAlaGlnGlyLeuTyr 217
Db 622 GTGGGAAACACACCGTCCCAAAAGTGAATGCTGCACTGCAAGACTGCAACTC--- 678
Qy 218 GlnGlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgGlyLeuGlu 237
Db 679 AGCCCGACGCTCAGATACGGCTTCTACCTCAGTCAAGAGAGCTCAGCCGATGGGCC 738
Qy 238 SerSerValThrGluPheIleSerArgGluTyrProAspSerGlnAlaProValThrGlu 257
Db 739 TGCGATTTTGACAGCTGATCTCCAAAGACTGCTCAATTTGACGATGACATTTCAAGC 798
Qy 258 IleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeu----- 275
Db 799 ATCTTAAGCCCAAGACAGAGAAATCTGTCTGTGCTGATGCTTGAAGCTGAAAGTC 858
Qy 276 -----GlySerValLeuAsnAsnAspThrLeuLeuGlyAspTyrAlaGluLeuGln 293
Db 859 CCACCTGGGGCGCTGATCCAGAC-----ATCTGGGGGACTGGAGAGAAAGAG 909
Qy 294 ProProPheThrLeuIleArgSerLeuLeuArgIleValLeuLeuProGluSerPheLeu 313
Db 910 CCGGTGCCCCCTCTCTGGGAGTTTGTCTGAAGAGAAAGATTATCCAGGGCGCCCTTG 969
Qy 314 IleValThrValArgAspValGlyThrGluLeuLeuSerGluValAlaSerProArg 333
Db 970 CTGGTCAACACGCGGCCAGGCACTGAGGAGACTTCCAGCTCTGGCGGACAGCCATC 1029
Qy 334 TyrLeuLeuValArgGlyIleSerGlyGlnGlnArgIleHisLeuLeuLeuArgGly 353
Db 1030 TAGCTAAGGCGTGAAGGCTTCTGGAAGAGACAGAGAGGCGCTATTTCTGAGACATTT 1089
Qy 354 IleGlyLeuHisGlnIleThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeu 373
Db 1090 GGAAGACAGACAGACAGCCATCGCTTGTAGCTAATGAGACCAACGCGCCCTGTC 1149
Qy 374 AspGlnCysGluValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAsp 393
Db 1150 CAGCTGGGCTGGCCCCCGGCTGTCTGATGTGTGTCACAGACTTGAAGCTGCAAGT 1209
Qy 394 ValValGlyLeuSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPhe 413

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Db 1210 GAGAAAGGGAGAGACCCGCTCCCACTGCTCAACCCGACAGGGCGCTGTTCTGCTTC 1269
Qy 414 ValPheHisGlnLeuThrProArgGlyValAlaArgArgCysLeuAsnLeuGluArg 433
Db 1270 CTCTGCAGCCGGTTC---CCGACAGGCGCA-----CAGCTGCGG 1305
Qy 434 ValValLeuLeuArgPheCysArgMetAlaValGlnGlyValIleTrpAsnArgIleSerVal 453
Db 1306 GCGCGCTGGGACGCTGAGCCCTTGGCCGCCACAGGCGCTGTGGCGCGAGATGCTCGTG 1365
Qy 454 PheAspGlyAspAspLeuMetValGlnGlyLeuGlyGlnSerGluLeuArgAlaLeuPhe 473
Db 1366 TTCACCGAAGACCTGGAAGGCTCGGGGTGCAAGAGTCCAGCTCCGCTGTTCTG 1425
Qy 474 HisMetAsnIleLeuLeuProAspSerHisCysGluGluTyrTyrThrPhePheHisLeu 493
Db 1426 GAGGAGACATCTCTCGCCAGACAGAGTCCAAAGCTGCTATCTTCATCCACTC 1485
Qy 494 SerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeuGlu----- 507
Db 1486 AGCTTCAGAGATTTCTCACTGCCCTGTCTACGCTCGAGAAAGAGAGAGGGGAGAC 1545
Qy 508 -----GlyLeuGluIleGluProAlaLeuCysProLeuTyrValGlyLeuThr 523
Db 1546 AGGACGCGCCACGCTGGGACATCGGGAGCTACAGAACTGCTTTCGAGAAAGAAAGA 1605
Qy 524 LeuArgSerMetGluLeuLeuGlnAlaGlyPheHisIleHisSerLeuTyrMetLeuArg 543
Db 1606 CTCAGAAACCCGACCTGATTCAGTAAAG-----CAC 1638
Qy 544 PheLeuPheGlyLeuValSerGluAspValAlaArgArgProLeuGluValLeuLeuGlyCys 563
Db 1639 TTTCTATTGCGCTCGCTGTAACAGAAAGAGCCAGAGAGATTGAGGCGCACTTTTGGCTGC 1698
Qy 564 ProValProLeuGlyValIleGlnIleLeuLeuHisIleTyr---ValSerLeuLeuGlyGln 582
Db 1699 CGGATGCACCGGACAGCAAAAGAAATTTCTGATGCAAGACACATCTTCAGCAAT 1758
Qy 583 GlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCysLeuPheGluThr 602
Db 1759 AAGCCCTTATCCGTAAC-----GACCTGAAGAGGCTTGGGGCTCCGTATGAGCTCT 1812
Qy 603 GlnAspLeuGluPheValArgLeuAlaLeuAsnSerPheGlnGluValIleProIle 622
Db 1813 CAGGAGAGAGCTGGCGGAAGTGTGTGCTGCCCTTCAAGAAATTTCTATTCACCTG 1872
Qy 623 AsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArg 642
Db 1873 ACAAACTCTTGAAAGATGCATTTGTTCTTCAGCTGAAAGCATGTGTCAAGACTTGAC 1932
Qy 643 LeuIleArgValAspVal---LysGlyIlePheProArgAspGluSerAlaGluAlaCys 661
Db 1933 AAATCTTCATCTGACAGGATGCAAAAGGGGTGTC----- 1965
Qy 662 ProValValProLeuTyrMetArgAspLeuThrLeuIleGluGlnIleTyrGluAspPhe 681
Db 1966 -----CTGAGAGATTACATGATTTT 1986
Qy 682 -----CysSerMetLeuGlyThrHisProHisIleuArgGlnLeuAspLeuGlySer 698
Db 1987 GAATCTGACATTTGAATTTGAAGCTCAAAACAGCACTTCAAGTTTCTGGAAGTAAACAA 2046
Qy 699 SerIleLeuThrGluArgAlaMetLeuThrLeuCysValAlaLeuAsnArgHisIleProThrCys 718
Db 2047 AGCTTCTGATGATCTTCTGTGCGGATTTCTTTGTACACAGTAACCCGTAGACCTGT 2106
Qy 719 LeuIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTyr 738
Db 2107 CATCTGAGAAAGTGAATTAATAAACCTCAACCCCTGACACCGGATCCGGGACTTCTGT 2166
Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisLeuLeu 758
Db 2167 CTTCCTTTCATTTGGAGAAAGACCTTCAGCACTGACCTTGGCAGGG---CACATCGAG 2223

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Qy	759	GlulgluAap-----ValAGMeAlaCyAgluAlaleuUysHl.sProlYsCyLeuUeu	776
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Qy	777	GlUsertleuAgtleuAapCy.sCyAglyLeuThrhIvalaCybTytleuUysIleserIn	796
Db	2284	CAGTAACCTGAGGTTGGAGAGTCACTGTGTCCACCCCGAGCAGTGGGGCTGAATTCCTTAT	2343
Qy	797	IleleuThrhTsrProserleuUysSerleuSerleuAlaGlyAsnUysValThrAsp	816
Db	2344	GTCCTCAAGCCCAACCACTCCCTTAAGCACTGGGGTCTCTAGCCMAATGCTCCTGAT	2403
Qy	817	GlInglyValMetProleuSerAspAlaleuUryalSerInCyvalAleuGlUlyleu	836
Db	2404	GAGGGTCGCAATTTGCTGTCTACAAACATGACAGCCCAAAACACTTCTGTCAATGTG	2463
Qy	837	IleleuGlUapCy.sGlyIleThralaThrslyCyvInserleuAlaSerAlaleuAl	856
Db	2464	TCTGTGAAACTGTGCTTCAACAGAACCAAGTTGCACAGACCTGTGCTGTGTGGT	2523
Qy	857	SerInaArgserleuThrhIleUysleuSerInAsnAsnSerleuGlYAsnGlUlyAl	876
Db	2524	GTCGACAAAGCTGACACACCTGTGCTGTGCACAAAGCCCATTTGGGGATACAGGGGTG	2583
Qy	877	AsnleuUeuCy.sArgserMetArgleuProHIsCySerleuGlInArgleuMetUasn	896
Db	2584	AAGTTTCTGTGTGAGGGCTTGAAGTTACCTGATTTAACTGCAGACCTTGGTGTGGTG	2643
Qy	897	GlInCybHIsleuAapThralaGlyCy.sGlyPheleuAlaleuAlaleuMetGlyAsnser	916
Db	2644	TCTTGTTCGGTACACACTCACAGAGGGCTGATCTCTCTTGGCCCTTGAAGTCAACAG	2703
Qy	917	TrpleuThrhIsleuSerleuSerMetAsnProValGlUAspAsnGlyValUlyleuUeu	936
Db	2704	TCCCTGAAGTGGTAAACCTCTCCACAAATAGCTTGGAAAGAGGGTCTAAGTTGCTG	2763
Qy	937	CyAgUValMetArggluProserCybHIsleuGlInAsnleuGlUleuValUlyeCybHIs	956
Db	2764	TACACACTTTCAGACACACCCCAAGTGTCTTCTGCAGAGTGTGTGTTGAAACCTGTAC	2823
Qy	957	LeuThralaAlaCy.sCyAgUserleuSerCyvalIleserArgserArgHIsleuUys	976
Db	2824	CTTACAGAAAGCCAAATTGCAGAGACTTGTCTGTGTGTGTGTCACGGGAGCTGCACA	2883
Qy	977	SerleuAapUleuThrAspAsnAlaleuUlyAsnGlyValAlaAlaleuCy.sGluUly	996
Db	2884	CACCTGTGCTGGCCCAAGAACCCCATTTGGAAATACAGAGGGTGAAGTTCTGTGTAGGGC	2943
Qy	997	LeuUysGlInUysAsnserValleuThrhArgleuGlyLeuUysAlaCy.sGlyLeuThrSer	1016
Db	2944	TTGAGAGTACCCCGAGTGTAACTGACAGACTTGTGTGTATACAGCATGACGATACAAAG	3003
Qy	1017	AspCy.sCy.sGluAlaleuSerleuAlaleuSerCy.sAsnAlaGlyHIsleuThrSerleuAsn	1033
Db	3004	CTTGGCTGTGAATATCTCTCAGAGCGCTGCCAAGAGCCTGACGCTCACAACCTGTGAC	3063
Qy	1037	LeuValGlInaAsnAsnPheSerProUysGlyMetMetUlyleuCy.sSerAlaPheAlaCy.s	1056
Db	3064	TTGAGTATCAACACAGATAGCT---GTTGATTTGTGAATTTCTGTCAAGCATTTAGAAAT	3122
Qy	1057	ProThrSerAsnleuGlIn 1062	
Db	3121	CCAAACGTAACTTAAA 3138	
RESULT 3			
US-11-136-527-4000			
; Sequence 4000, Application US/11136527			
; Publication No. US20050287570A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William M			
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes			

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FILE REFERENCE: 031896-04100 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4000
LENGTH: 5100
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-4000

Alignment Scores:
Score: 5.12e-78
Score: 957.00
Percent Similarity: 36.15%
Best local Similarity: 23.83%
Query Match: 13.53%
DB: 8
Gaps: 55

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US-10-066-521-6 (1-1344) x US-11-136-527-4000 (1-5100)

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Oy 30 LysGluLeuLeuLysLysLysSer---SerGluSerThrTrpCysSerIleProGlnPhe 48  
Db 232 CAGCTTCTGCTGGCAATTAAAGCGACCTCCAGAGAGCTTTGGGTGAAGACACCGCTCAG 291  
Oy 49 GluIleGluAsnAlaIasnValGluCysLeuAlaLeuLeuLeuHISGluTyrTyrGlyAla 68  
Db 292 CCAGAGAAACAGATGGCATGGAGGTGGCTGTACTCTGGTGGCTCAG---TATGGGAG 348  
Oy 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuAlaTyrThrLeuSer 88  
Db 349 CAGGGGGCGTGGGACCTAGCCTCATATCGGAGGACGATGGGGCTGAAGGTCACTGTGC 408  
Oy 89 GluLysAlaIaArgAsp----- 93  
Db 409 GCCCAAGCCGAGGAAGGGGAGGCCCATCTCTCTCATTCCTCCAGCCAAAGTAAACC 468  
Oy 93 ----- 93  
Db 469 CACCTGGGCTTCCAGCCAAACCACCTCCACCGCAGTCTAATGCCCTGGATCATGAA 528  
Oy 94 -----AspMetLysLysIleSerGlnAlaMetGluGln 104  
Db 529 TTGCCGGCGGGGTCACCCAGGGCTCAGAGAGAAAGGTTTGAACACAGCTGCCGACACA 588  
Oy 105 GluGlyAlaIaThrAlaIaGluThrGluGluGluGlnIleSerGlnAlaMet----- 121  
Db 589 TCTGGACGCGCTGAGAGAAATCTGTGCTCTACACCTCTACCAAGCTTCCAAAGCTCC 648  
Oy 121 ----- 121  
Db 649 CCAGACCATGAGTCTCCAAAGCAGAGATGCCAAAGCCCCACATCCACAGAGTCTG 708  
Oy 122 -----GluGlnGluGly----- 125  
Db 709 GGGAGCTGGGAGATCCCACTCAGGCCCAGCCTAGACCCCAAGAGCAGAGAGCTCTGGG 766  
Oy 125 ----- 125  
Db 769 ACCCAATGGCTGTGATGATAACGTCAAGAAATTACTACACAGAAATCAGAGAAAGAG 828  
Oy 126 -----AlaThrAlaIaGluThrGluGln 134  
Db 829 AGAGAGAAATCAGAGAAAGCAGAGCCCCCATGGGACGGGTGTAGAGAAAGCCCCCAG 888  
Oy 135 GlyHisGlyGly----- 138

Db 889 GCGCAGCAGCAGCCTACAGCCCAACCAACCCATGGAGCCTTCTGTGAGAGAGAGCCTC 948  
 Qy 139 ---AspThrTrpAspTyrTyrSerHisValMetThr---LysPhe----- 151  
 Db 949 TGTTCACATAGCCCTGGAAAATGAGGATTTTAAACCAAAAATTTCACACAGCTCTACTT 1008  
 Qy 152 -----AlaGluGluGluAspValArgArgSerPheGluAsnThr 164  
 Db 1009 CTACAAAGACCTCAACCCAGAGCCAGATCCCTGGTCAAGAGAGAC----- 1056  
 Qy 165 AlaAlaAspTrpPro-----GluMetGlnThr 173  
 Db 1057 -----TGGCCTGATTATGTGAGAGAGATGAGAGACATTTAATTTAGATGAGAC 1107  
 Qy 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeu 192  
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 Qy 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAla 212  
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 Qy 213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232  
 Db 1216 AGAGCCAGCTGTAATGGGAGCCGCTTCAGCATGCTTTTCACTTCACTGAGAGAGCTG 1275  
 Qy 233 GlnArgLysLysGlySerSerValThrGluPheIleSerArgGluTrpProAspSerGln 252  
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 Qy 253 AlaProValThrGluIleMetSerArgProGluArgLeuPheIleIleAspGlyPhe 272  
 Db 1336 GCTCCCATTTAGACAGATCTGTCTAGCCAGAGCGGCTGCTTCATCTCGATGGTGTA 1395  
 Qy 273 AsnAspLeuGlySerValIleAsnAsn---AspThrTyrIleuCysLysAspTrpAlaGlu 291  
 Db 1396 GATGAGCAGAGATGGGTCTTGACAGAGCCGAGTTCTGACCTGTCTGCACTGGAGCAG 1455  
 Qy 292 LysGlnProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSer 311  
 Db 1456 CCACAGCCGGCGAGTGCATGCTGGGCAATTTGCTGGGAAAATATATATCTCCGAGGCA 1515  
 Qy 312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGlnValSer 331  
 Db 1516 TCCTTTGTATACAGGCTCGGACCAACAGCTCTGAGAACTCATTCCTTTGAGACAG 1575  
 Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGlu 351  
 Db 1576 GCAGGTGGGTAGAGGTCTGGGGTCTCTGATCCAGCAGAGAAATATTTCTACAGA 1635  
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 Qy 372 LeuLeuAspGlnCysGlnValProAlaValIleLysLeuIleCysValAlaLeuGlnLeu 391  
 Db 1696 CTGGGGCCCTGTGTCTTGTGGCTGGGTGTCTGGCTGGCTGCACCTGGCTGATGACAG 1755  
 Qy 392 GlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrGly-----Leu 409  
 Db 1756 CAGATGAGCGGAGGAGAAAATCACACTGACTTCAGAGACACACCAACCCCTGTGCTTA 1815  
 Qy 410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsn 429  
 Db 1816 CATTAACCTGGCCAGGCTCTCCAGCTCAGCCATTGGGA----- 1854  
 Qy 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449  
 Db 1855 -----CCCAAGCTCAGAGACCTGTGCTGTGGCTGTGAGGGAGGATGTGGCAA 1902  
 Qy 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGluLeu 469  
 Db 1903 AAAAAGACCTTTTCACTGCCAGATGACCTCAGAGAGATGGGTGTAATGGGGCCATCATC 1962

Qy 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGlu 485  
 Db 1963 TCACACCTTTGTAAGATGGGATTTCTTCAAGAGAGACCCCATCCCTCGAAC----- 2013  
 Qy 486 GluTyrTrpThrPhePheHisLeuSerLeuGlnAspPheCysValAlaLeuTyrTyrVal 505  
 Db 2014 -----TACAGCTTCATTCACCTCTGTTCACAGAGTTCTTTTCAGCAAGATCCCTATGCT 2067  
 Qy 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCysProLeuTyrValGluLysThr 523  
 Db 2068 TTGAGAGATGAGAGGGGAGAGAGTAAACATTTAATTGATCATAGATTTGGAAAAGACG 2127  
 Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540  
 Db 2128 CTGAAGACA-----TATGAAATATACAGCCCTGTTGGGGCATCA 2166  
 Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560  
 Db 2167 ACCACAGCTTCTTATGGGCTGTAAATGATGAGGGGAGAGAGAGATGAGAGACATC 2226  
 Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisTrpValSerLeuLeu 580  
 Db 2227 TTTCACCTGCCGCTGTCTCAGGG-----AGAACTTATGCCAGTGGTCCGCTCCTT 2280  
 Qy 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598  
 Db 2281 CAGCTGCTGTGCAGCCACAC-----TCTCTGAGTCCCTTCACCTGC 2322  
 Qy 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618  
 Db 2323 TTGATATGAGCTCGAACAACGATTCCTGACACAGTGTAGGCCCATTTTCGAAGAAATG 2382  
 Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638  
 Db 2383 GGCATGTGTATGAACAGACATGAGACTTATGTGTCACCTTCTGATTAATTTGAC 2442  
 Qy 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGlnSerAla 658  
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 Qy 659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGlnTrp 678  
 Db 2491 ACATGAGCCCAAGCAGATGATCTCTGTCAGAGTGGTCCCACTGACAGATGCCATATTGG 2550  
 Qy 679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698  
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 Qy 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738  
 Db 2551 -----CAGATTCTTCTTCC 2562  
 Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLys 758  
 Db 2563 TCCGTCTCAAGGTCAACCAAACTTAAGAGAGCTGAACCTTAATGGAACCTGCTAGAC 2622  
 Qy 759 GluGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGlnSer 778  
 Db 2623 CACTGTCAATGAAGAGCTTTGTGAAGACCTGAGAGCCCTGCGTGCCTCGTAGAC 2682  
 Qy 779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeu 798  
 Db 2683 CTGGCG----- 2688  
 Qy 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyLysAsnLysValThrAspGlnGly 818  
 Db 2689 -----TGGCTGGC----- 2697

QY 819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuLeu 838  
 Db 2697 ----- 2697  
 QY 839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858  
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 QY 859 ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeu 878  
 Db 2752 CAGACC----- 2757  
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 Db 2757 ----- 2757  
 QY 899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeu 918  
 Db 2758 -----CTG 2760  
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 Db 2761 ACCGAGCTGAGACTGATGCTTCATGCTGCTCATGATGCTGAGCCAAACACCTTTGGCCAG 2820  
 QY 939 ValMetArgGluProSerCysHisLeuGlnAspLeuGlnLeuValLysCysHisLeuThr 958  
 Db 2821 AGACTGAGACAGCCGAGCTGACAGCTACAGCACTGACGCTGGTGTAGCTGTGGCTCAGC 2880  
 QY 959 AlaAlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978  
 Db 2881 TCTGACTCTCCGACGAGCTGCGCTGTGCTTACTGACAGCCCAAGCTGAAAGAGCTA 2940  
 QY 979 AspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlnGlyLeuLys 998  
 Db 2941 GACCTGACGACGAAACAACTGATGACCTGGCTGGCCACCTGCTCTGTGAGGGGCTCAG 3000  
 QY 999 GlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCys 1018  
 Db 3001 CATCTGCTGCCTGCAAACTCATACGCTGGGCTGACACAGACACTGTAGTATAGATG 3060  
 QY 1019 CysGlnAlaLeu-----SerLeuAlaLeuSerCysAsnArg 1030  
 Db 3061 AGGCAAGGAGCTGAGGGCCCTGGAGAGAGAGAACTCAGCTGCTCATCTTACGACAGCG 3120  
 QY 1031 HisLeuThrSerLeuAsnLeuValGln-----AsnAsnPhe 1042  
 Db 3121 AAACCAAGTGTGATGACCCCTATTGAGGGCTGTGATACGGAGAGATGATGATACACA 3180  
 QY 1043 SerProLysGlyMetMetLysLeuCysSerAlaPheAlaCys-----ProThrSer 1059  
 Db 3181 TCCCTCACTCAAGCGGACGAGACTCGATCAGAGAGGGCGGCTTCCCATGTTCTCAAGCT 3240  
 QY 1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnLysProValGlnIleArgLysLeuLeu 1079  
 Db 3241 AATCTCAAACTCTGAGAGCTGAGCAAG--ATCTTCCA-----ATTCTGAAGATGCA 3291  
 QY 1080 GluGlu-----ValGlnLeuLeu--LysProArgValValIle 1091  
 Db 3292 GAGGAAGAGCTCCCAAGAGGTAGTACCGGTGAACCTTGTGCGTCTTCTCTGCTCTCT 3351  
 QY 1092 AspGlySerTrpHisSer-----PheAspGluAsp----- 1101  
 Db 3352 CAAGGGAGACTGCATACGAAGCCTTTGGGAGCTGACGATGACTTCTGGGGCCCAAGGGG 3411  
 QY 1102 -----AspArgHisLysIleGlyLeuThrPheArgLeuProGlu 1114  
 Db 3412 CCTGGGCTACTGAGGTACTTACAAAGAAAGAACTT-GTACCAAGTTCATCTCCCTCT 3470  
 QY 1115 SerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProGlnGlnLysLysArgVal 1134  
 Db 3471 AGCTGGCTCTCAACCGCTGCC-----CAACACGGG 3500  
 QY 1135 SerLeuLeuAlaGlyAspPheLysSerSerThrArgPheAlaLysSerLeuCysLeuAla 1154

Db 3501 TCTTGTCTTGTGTGTGAG--AGAGCGGTGACCGTTGAGATTGAATTTGTGTGTGGGA 3557  
 QY 1155 ThrAlaAsnGlyLysArgGlnArgValAspAsnValGluGlnSerSerProGlnPromet 1174  
 Db 3558 CCAATTCCTGGGTGAGATCAA----- 3578  
 QY 1175 AlaGlyThrGluHisLysGlnAspLysMetLeuSerValGlyTyrSerGlyAlaTrpSer 1194  
 Db 3578 ----- 3578  
 QY 1195 GluThrAlaGluLeuGlnGlyLysLeuGlySerAsnSerAlaAspHisLeuGlyMet 1214  
 Db 3579 CCCACAGCAGCAGCTGAGATGT--GCGAGGGCCCTGCTGAGACATCAA--GGCTGA 3629  
 QY 1215 AlaTrpSerLeuGlyArgGlnLeuSerSerArgLysCys-----ProThrValLeu 1232  
 Db 3630 GCTTGAGACCGGTGA--AGCTGTGACACTTCCCTCATTGTGGCTCTCCAAAGGGG-GCC 3685  
 QY 1233 MetThrThrAlaValCysProGlyHisTrpGluArgLeuGlySerArgLys----- 1249  
 Db 3686 ATGTGACACATCCCTGT--TCCAGTGGCCCACTTTAAAGAGAGGGAGATGCTCTGG 3742  
 QY 1249 ----- 1249  
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 QY 1250 -----Trp 1250  
 Db 3803 TGGAGTCTCTGTGAAATGATCATATAGCTTGGCTGCTTATCCCTCACTGTGTGG 3862  
 QY 1251 Cys-----LeuAsnSerAlaAspAsnHisSer----- 1259  
 Db 3863 TGTGCTTTACACCGCTCCATCTGTAGAAAGTACACTTCCACTCACTGATCCCA 3922  
 QY 1260 -----GlyValSerTrpSerLeuGlyAlaGlyLeuGlnGlyLeuVal 1274  
 Db 3923 GTGACTGCTCCATTGCGAAGAGACTGAGC-----TGTGATATGAAAGCCCTGGAG 3973  
 QY 1275 SerAsnSerAlaAspAspHisSerGlyValAla-----TrpSerLeuGlyValAla----- 1291  
 Db 3974 AAGACACACTGTTCTCGAGTTTCTAGTGGCCACTTGGACATCGAGATCGAGCTGCAAG 4033  
 QY 1292 -----GlyLeuGlnGlyLeu----- 1296  
 Db 4034 TGAAGACAAAGAAATGAGACTGTGTGTGGAGGCTTGGTGAACAGGAGATCTCA 4093  
 QY 1297 -----ValSerAsnSerAlaAspAspHisSerGly-----ValSerTrpSerLe 1311  
 Db 4094 TGCCTGCAACTGATCTGATTCCTCCAGCCTGATGCGGTACCTTCACTCTGATGCC 4153  
 QY 1311 uGlyAlaAlaGlyLeuGlnGlyLysLeuValSerAsnSerAlaAspAspHisSerGlyValSe 1331  
 Db 4154 CGCACTGTCTGCACTTGTGTGACAGTATCGAGACAGCTGATACCCGAGTACATCGG 4213  
 QY 1331 rTrpSerLeu 1334  
 Db 4214 -TGAAGGTTG 4222  
 RESULT 4  
 US-11-136-527-4006  
 ; Sequence 4006, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; PRIOR FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 362830



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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4006
; LENGTH: 4390
; TYPE: DNA
; ORGANISM: Rattus norvegicus
;
US-11-136-527-4006

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Alignment Scores:	
Pred. No.:	1,49e-22
Score:	364.00
Percent Similarity:	36.588
Best Local Similarity:	22.928
Query Match:	5.15%
DB:	8
	Gaps: 60
	Length: 4390
	Matches: 287
	Conservative: 171
	Mismatches: 454
	Indels: 342
	Gaps: 60

US-10-066-521-6 (1-1344) X US-11-136-527-4006 (1-4390)

QY	189	ThrValValLeuHisGlyLysSerGlyTLeGlyLysSerAlaLeuAlaArgArgTLeVal	208
Db	1013	ACCAATCTTCAATCCCGGGGATGATCGGGGGGGCAAGTCAATGCTCAAGCCGGCTGAG	1072
QY	209	LeuCySTPrAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuPro	228
Db	1073	AGCCTGAGGGCAGAGGGCGGCTGAGCAGAGGGGTC---AAATTCTTCTCACTTCCG	1129
QY	229	ValArgLeuMetGlnArgLysLysGlyLysSer-----ValThrGlnPheIleSer	245
Db	1130	TGCAGCATGTTCAGCTGCTTCAGAGAAAGTCAAGAGCTGTCTGCGAGAGCTCTCTTC	1189
QY	246	ArgGluTrpP-----ProAspSerGlnAlaProValThrGluIleMetSerArg	261
Db	1190	AAGACATCACTCACTCAAGAGCGGAGCCCAAGAGAGGTGGTTGGCTCTCTGCGCTTC	1249
QY	262	ProGluArgLeuLeuPheIleIleAspGlyPheAspPheLeuGlySerValLeuAsnAsn	281
Db	1250	CCCCACGGCGCCTTCACTCACTTCGATGGCTTGAGACAGACTGTCACCTCGAATTTG--	1303
QY	282	AspThrLysLeuCyLysAsp-----ThrAlaGlyLysGlnProProPheThr	297
Db	1304	GACCTGAGCGCGGTGCTGACAGACTCTGCCCCCTGG---GAGCCTGCCACCCCTGGCTC	1360
QY	298	LeuIleArgSerLeuLeuArgLysValLeuLeuProGlnSerPheLeuIleValThrVal	317
Db	1361	TTTGTGTGGCAACCTGTCTCACTAGTGGAGAGCTGTCAAGGGGGCTTACAGACTGTCTCAAGCC	1420
QY	318	Arg-----AspValGlyThrGlnLysLeuLysSerGlnValValSerProArgTyr	334
Db	1421	CGCAGAGGATCGAAGTCCCGCGCGACAGTTCTCGCGAAAGAGTG-----	1465
QY	335	LeuLeuValArgGlyLysSerGlyGlnArgLysIleIleLeu-----	348
Db	1466	---CTTCTCCGGGGCTTCTCCCCAGC-----CACCTGGCGGCTATGCCAGAGG	1513
QY	349	---LeuLeuGlnArgGlyLysGlyLysIleGlnLysGlnLysThrGlnGlyLeuArgAlaIleMet	367
Db	1514	ATGTTCCTCCGAGCGGGCGCTTCAGAGACCGGCTGCGAGCGAG-----CTGGAG	1561
QY	368	AsnAsnAsnArgLysLeuLeuAspGlnCySerGlnValProAlaValGlySerLeuIleCyVal	387
Db	1562	GCCAAACCCCAACTGTGAGCGCTGTGCTGTGCCC-----CTCTCTGTGCTGG	1609
QY	388	AlaLeu-----GlnLeuGln	392
Db	1610	ATCATCTTCCGAGTCTTCCAGACACTCCGAGTGGCTTTGAAGGCTCAACCAAGCTGCC	1669
QY	393	AspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrGlyLeuIleAlaAla	412
Db	1670	GACTGGC-----ACATGATCCCTGACAGAGATGTTCTCTCTGG	1705
QY	413	PheVal-----PheHisGlnLeuThrProArgGlyValValAlaGlnGlyLeuAsn	429
Db	1706	GTCACTAGAGTCACTCTGAAACAGATGACGCGACGCAAGCTGGTGGACGG---AAC	1759



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Db 2725 GATACCGATGTCGAGCAGTAGTCACCAAAATCTGGATGATGCAAAAGGCTCAC 2784
Qy 748 gSerLeuAsnLeuGlyThrHisLeuLysGluLysPheValArgMetAlaCysGluAl 768
Db 2785 GCATCTTAACTGGGAAAAAACAATAACAAGTAAAGAGGAGATCTCGCCCTGAC 2844
Qy 768 aLeuLysHisProLysCysLeuLeuGluSerLeuArgLeuSerCysGlyLeuThrHis 788
Db 2845 TGTGAAGAACAGCAAA----- 2860
Qy 788 aAlaCysThrLeuLysHisSerGlnIleLeuThrHisSerProSerLeuLysSerLeu 808
Db 2861 -----TCAACTCTGAGAGTTGG 2877
Qy 808 rLeuAlaGlyLysLeuValThrArgGlnGlyValMetProLeuSerArgPheAlaLeuArgVa 828
Db 2878 GATGTGGGCAATCAAGTTGGGATGAAGAGCAAAAGCCTTCGACAGGCTCTGCGG-- 2935
Qy 828 lSerGlnCysAlaLeuGlnLysLeuLysLeuGluLysArgCysGlyIleThrAlaThrGlyCy 848
Db 2936 -AACACACCCAGCTTGACCAACCTGAGTCTTCGCTCAACGCACTTCACAGAGAGG 2994
Qy 848 eGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAs 868
Db 2995 AAAGAGCCTTGCGAGGCGCTTCGACAGAAACAGTCTCTAAGAAATCTGTGCTGACCCA 3054
Qy 868 nAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetAlaGluProHisCy 888
Db 3055 AAATCAACTCAACAGTGAAGTGGCAGAGAGTTGGCAGAAATGTTGAAAGTC--AACCA 3111
Qy 888 sSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLe 908
Db 3112 GACGTTAAAGCATTTATGCTTATCCAGAAATCAAGTACAGTAAAGGAGGACCTGCCAGT 3171
Qy 908 uAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProVa 928
Db 3172 GGCAGATCGTTTACAGAGCAACACTGGCATACAGAGATTGCTTAATGAAACCTGAT 3231
Qy 928 lGluAspAsnGlyValLysLeuLeuCysGlyValMetArgGluProSerCysHisLeuGlu 948
Db 3232 AAAACAGAGAGGCGCAAAAGTCTAT--GAAAGTAAAGAGCGGATTAATCTGTTTGTGAGA 3288
Qy 948 nAsp-----LeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSe 964
Db 3289 GGATCTCTTCTGTTCAATGGGGTTTGGCTTCGAGACCTCAGACAGCAAAATGCCACTCG 3348
Qy 964 rLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAl 984
Db 3349 GCAAGCTTTTGTGTCAAGTGTCTTAAAGGGGCTGCGAGGCGGAGCTATCAGAGATGCAC 3408
Qy 984 aLeuGlyAspGlyGlyValAlaAlaLeuCys-GlnGlyLeuLysGlnLysAsnSerValL 1004
Db 3409 TGCCCTCATGATGACAAGCAAGCTTCCTGCGAAGAGTCTGTGCTCGGCAAA-----C 3459
Qy 1004 euthArgLeuGlyLeuLysAlaCysGly-----LeuThrSerAspCysCys---- 1019
Db 3460 TCCCTAAGTACCCGCTACATTCCTGACAAAAAAGATGTCTCTGAGAGCTGTGATGTT 3519
Qy 1020 -----GluAlaL 1022
Db 3520 ACAGTAATATACACTGGAAGAGACTTATGCTATTAATATTTTATCTGAAGCTA 3579
Qy 1022 eusSerLeuAlaLeuSerCysAsnArg-----HisLeuThrSerLeuAsnLeuV 1038
Db 3580 GAGGATTAAGCTGTGAGCAAAACAGAGAGGCGAGCCTCACTCATCTCAACAGACTGCCA 3639
Qy 1038 aGlnAspAsnPheSerProLysGlyMetMetLysLeuSerAlaPheAlaCysProt 1058
Db 3640 TAGGAGCAACGAGGAGC-----GAGTTGGTCAACCGCTCTTTTC----- 3677
Qy 1058 hrSerAsnLeuGlnIleLeuGlyLeuTrpLysTrpGlnTrpValGlnIleArgVal 1078

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Qy 1078 eLeuGlu-----GluValGlnLeuLeuLys----- 1086
Db 3718 TTTCTGAATTAAGCTGTTTGAATGATGATTAATTAATTAATTAATTTCTCTCTC 3777
Qy 1087 -----ProArgValValIleAspGlySerTrpHisSerPheAspGluAspArgH 1104
Db 3778 AGCACTTTCCCAT--GTATGTATCTAGTGTGCCCATTCACAGCTCG-----AGAC 3824
Qy 1104 lLysIleGlyLeuThrPheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuT 1124
Db 3825 ACCGAGATATGTCAGTGTGGATTTGACTCTCCAG-----GTTTTGT 3869
Qy 1124 rPglYMetAsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAspPheLysSer 1144
Db 3870 CGAAAGTTAAATGTCAAGAAAGATGACACAGCGCTTTAATTTAATTCCTGAGTCTC 3929
Qy 1144 eThrArgPheAlaLysSer-----Leuc 1152
Db 3930 ACTGTCTGTGGCAAAAGATAGAGATGCTCAGCTCTTAAGTCTTAAGATGACAT 3989
Qy 1152 yLeuAlaThrAlaAsnGlyGluSerGlnArgValAspAsnValGluGlnSerSerProG 1172
Db 3990 GCTTTCAAAATGCT--GCTTCACACTAGGCGCTTCTCTGCTAGCTACCTCTCTTA 4046
Qy 1172 lProMetAlaGlyThrGluHisLys-----GlnAspLysMetLeuSerValG 1188
Db 4047 GAAAGCTAGTACCACTAGGCGCTACACTGTCTGCGCTTGGGAAGAAATGATTTGTCTCC 4106
Qy 1188 lYTrSerGlyAlaTrp----- 1193
Db 4107 AAAGAAATAGGCAATGAGCTGCGCTGCGCTGCGCTGCGCTCAATAGCTGTTGTCTC 4166
Qy 1194 -----SerGluThrAlaGlu-----LeuG 1200
Db 4167 CCTTACTCTGTGAAGAGGAGAGTCTTCTGCTGCTCCACAGCACTTAAGGCTGATCA 4226
Qy 1200 lGluGly-----LeuGlySerAsnSerAlaAspHis--AspHisG 1212
Db 4227 ACGGCGCGAAGACTCAGAGGATGGCTTGGAACTGGCGCCAGCAGACATGTTGGACACC 4286
Qy 1212 lYgIyMetAlaTrpSerLeuGly-----ArgG 1221
Db 4287 CCCCAACATGGTGGCTGTGTGTGCTGCTCATGAGGATGGGGGTGATTAATAATGATC 4346
Qy 1221 luleuSerSerArgGlyLeuCysProThrVal 1231
Db 4347 ACTTGTCTCT-----TGCCCGCTCAT 4369

RESULT 5
US-10-966-846-1
/ Sequence 1, Application US/10966846
/ Publication No. US20050287612A1
/ GENERAL INFORMATION:
/ APPLICANT: Bertin, John
/ APPLICANT: Philpott, Dana
/ APPLICANT: Sansonetti, Philippe
/ APPLICANT: Girardin, Stephen
/ TITLE OF INVENTION: CARD-4 MOLECULES AND USES THEREOF
/ FILE REFERENCE: 07334-371004
/ CURRENT APPLICATION NUMBER: US/10/966,846
/ PRIOR APPLICATION NUMBER: US 10/706,857
/ PRIOR FILING DATE: 2003-11-12
/ PRIOR APPLICATION NUMBER: US 10/352,381
/ PRIOR FILING DATE: 2003-01-27
/ PRIOR APPLICATION NUMBER: US 10/154,485
/ PRIOR FILING DATE: 2002-05-22
/ PRIOR APPLICATION NUMBER: US 10/027,881
/ PRIOR FILING DATE: 2001-12-20
/ PRIOR APPLICATION NUMBER: US 60/258,724
/ PRIOR FILING DATE: 2000-12-29

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NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 3382  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (245) ... (3103)  
 US-10-966-846-1

Alignment Scores:  
 Pred. No.: 2,566-22 Length: 3382  
 Score: 359.50 Matches: 225  
 Percent Similarity: 38.30% Conservation: 135  
 Best Local Similarity: 23.94% Mismatches: 367  
 Query Match: 5.08% Indels: 214  
 DB: Gaps: 41

US-10-066-521-6 (1-1344) x US-10-966-846-1 (1-3382)

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 209 LeuCystrPalaGlnGlyLysLeuTyrGlnGlyMetPheSerTyrValPhePheLeuPro 228  
 893 AGCCTCTGGGCGACGGGCGGCTGAGACGAGGGGTC--AAATCTTCTTCCACTTCCG 949  
 229 ValArgLysMetGlnArgLysLysLysSer-----ValTrpGlnPheLeuSer 245  
 950 TGGCGGATGTTACAGCTGCTTCAAGAAAGTACAGCGGTGTGTGACAGACCTGCTCTTC 1009  
 246 ArgGlnTrp-----ProAspSerGlnAlaProValTrpGlnLeuMetSerArg 261  
 1010 AAGCACTACTGCTTACCCAGACGGGACCCGAGGAGGTGTTCCTTCTGCTGCGCTTC 1069  
 262 ProGlnArgLeuLeuPheLeuLeuAspGlyPheAspAspLeuGlySerValLeuAsn 281  
 1070 CCCACGTGGCCCTCTTCACTTCACTTCACTGCTGAGCTGCACTGCACTGCACTG 1123  
 282 AspThrLysLeuCyLysAsp-----TrpAlaGlnLysGlnProProPheThr 297  
 1124 GACCTGAGCGCGGTGCTGACAGCTCTGCGCTGCG--GAGCTGCGCCACCCCTGAGTC 1180  
 298 LeuLeuArgSerLeuLeuArgLysValLeuLeuProGlnSerPheLeuLeuValThrVal 317  
 1181 TTGCTGGCCACCTGCTCAGTGGAGAGCTGCTCAAGGGGCTGACCAAGCTGCTCAGAGCC 1240  
 318 Arg-----AspValGlyThrGlnLysLeuLysSerGlnValValSerProArgTyr 334  
 1241 CGCAGAGCATCGAGGTCCGCGCCAGATCTCTGCGGAAGAGTG----- 1285  
 335 LeuLeuValArgGlyLysSerGlyLysGlnArgGlyLeu----- 348  
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 349 ---LeuLeuGlnArgGlyLysGlyLeuHisGlnLysThrGlnGlyLeuArgAlaIleMet 367  
 1334 ATGTTCCTCCGACGGGCGGCTGACAGACCGCTGCTGAGCCAG-----CTGAG 1381  
 368 AsnAsnArgGlnLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysVal 387  
 1382 GCCAACCCCAACCTTGCAGGCTGTGCTGTGCCC-----CTTCTTCTGCTGG 1429  
 388 AlaLeu-----GlnLeuGln 392  
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 516 ---CysProLeuTyrValGlnLysThrLysArgSerMetGluLe 529  
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 2032 GTCCAAAGCCAAACAGAAAGCTCGCGGCAATGTGTGTCGGCG--GACAGCTGAGAG 2088  
 569 LysGlnLysLeuLeuHisIleTrpValSerLeuLeuGlyGlnGlnProAsn-----AlaThr 587  
 2089 AAGCGCAGAGCCCTG---TGGGCACACCTGTTTTCCAGCCTGCGGGGCTAAGAG 2145  
 587 rTrpProGlyAspThrLeuAspAlaPheHis----- 597  
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 2206 GATGCTGCGCTGATCTACAGAGACACAGGCCAGAAAGTGGGCGACCTGCGCGCCAGGG 2265  
 614 rPheGlnGlnValTrpLeuProIleAsnGln-----AsnLeuAspLeuIleAl 630  
 2266 CATTCGCGCAACATCACTCAAGCTCACTGACAGCTGACAGCTGCGCCAGCTGACAGCGC 2325  
 630 AspSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgValAspValVal 650  
 2326 CTTCTCTTGTCTGCTGATCACTTCTCC-----AAGCGGTGCGCTTACAGCTTACAGCAA 2379  
 650 yIlePheProArgAspLysSerAlaGlnAlaCysProValValProLeuTrpMetArgAs 670  
 2380 CAACAACTCAACAGACTACAGCGGTGGG-----GAGCTGAGGCGCTTCAAGCCGC-- 2431  
 670 PysThrLeuIleGlnGlnGlnTrpGlnAspPheCysSerMetLeuGlyThrHisProHis 690  
 2431 ----- 2431  
 690 GluLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetLysThrLeuCy 710  
 2432 -CTCACTGTTCTTCACTCAAGCTTAAACAGATGAGCGGTGGGTAAAGGTGCTTAAG 2490  
 710 sAlaLysLeuArgHisProThrCysLysLysIleGlnThr---LeuMetPheArgAsnAlaG 729

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Db      2491 CGAAGACTG-----ACCAATACAAATGTGTGACCTATTGGGTTTATACACACACCA 2544
Qy      729 nileThPro---GlyValGlnHisLeuThrPargIleValMetAlaAsnArgAsnLeuAr 748
Db      2545 GATCGCCGATGTCCGAGCCAGATGATGATCCAAATATCTGGATGATGATCCAAAGGCTTAC 2604
Qy      748 gserLeuAsnLeuGlyIleThrHisLeuLeuGlyIleValAspValArgMetAlaCysGluVal 768
Db      2605 GCATCTTTAACTGGGAAAAAACAATAACAAGTGAAGAGAGAGAGATCTCGCCCTGAC 2664
Qy      768 aLeuLeuHisLeuProlCysLeuLeuGluSerLeuArgLeuAspCysGlyLeuThrHis 788
Db      2665 TGTGAAGAACAGCAAA----- 2680
Qy      788 sAlaCysLeuLeuLeuSerGlnIleLeuThrThrSerProSerLeuLeuSerLeuSe 808
Db      2681 -----TCAATCTCGAGGTTGG 2697
Qy      808 rLeuValGlyValAsnLeuValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVa 828
Db      2698 GATGTGGGCAATCAAGTTGGGAGTGAAGAGCAAAACCTTCGACAGGCTCTGCGG-- 2755
Qy      828 lSerGlnCysAlaLeuGlnLeuLeuLeuLeuAspCysGlyIleThrAlaThrGlyCy 848
Db      2756 -AACCAACCCAGCTTGACCACTGATGCTTGCCTCCCAACGCGCATCTCCACAGAGAGAG 2814
Qy      848 sGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAs 868
Db      2815 AAGAGGCTTCGAGGCGCTCGACAGACACGCTCTTGAAGATACGTGTGCTTACCA 2874
Qy      868 nAsnSerLeuGlyValAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuProHisCy 888
Db      2875 AATGAATCTCAACATGAGTGAAGTGGCAGAGAGTTGGCAAAATGTTGAAAGTC--AACCA 2931
Qy      888 sSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuThrAlaGlyCysGlyPheIse 908
Db      2932 GACGTTAAAGCATTTATGCTTATCCAGATCAATCAAGTCAAGGAGGACTGCCACACT 2991
Qy      908 uAlaLeuAlaLeuMetGlyValAsnSerTrpLeuThrHisLeuSerLeuSerMetAspProVa 928
Db      2992 GCGCAGATCCGTTTACAGACCAACACTGCATACAGAGATTTGCTTAATGAGAACTTGA 3051
Qy      928 lGluAspAsnGlyValLeuLeuLeuCysGlyValMetArgGluProSerCysHisLeuGln 948
Db      3052 AAACACAGAGAGGCGCAAAAGTTAT--GAGATGAGAAAGCGGATTAATCTTTTCTGAGA 3108
Qy      948 nAsp-----LeuGluLeuValLeuCysHisLeuThrAlaAlaCysCysGluSe 964
Db      3109 GAGTCTCTTCCGTTTCATGAGGGGTTTGGCCCTCGAGGCTCAGACAGCAATGCCACTCGG 3168
Qy      964 rLeuSerCysValIleSerArgSerArgHisLeuLeuSerLeuAspLeuThrAspAsnAl 984
Db      3169 GCAGCTTTTGTGTGATGCTTTAAAGGGGCTCGGAGCGGCGGACTATACAGAGATCTCCAC 3228
Qy      984 aLeuGlyAspGlyGlyValAlaAlaLeuCysGlnGlyLeuLeuGlnLeuAsnSerVal 1004
Db      3229 TGCCTTCATGATGACAGCGAGGCTTCCTGTGCAAGAGGTGTGTCGCAAA-----C 3279
Qy      1004 eUTHrArgLeuGlyLeuLeuValAlaCysGly-----LeuThrSerAspCysGly 1019
Db      3280 TCCCTTAAGTACCCGCTTACATTCGTGCAAGAAAGAAATGTGTCTGAGAGCTTTGT 3335

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RESULT 6
US-10-966-846-3
; Sequence 3, Application US/10966846
; Publication No. US20050287612A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Philpott, Dana
; APPLICANT: Sansonetti, Philippe
; APPLICANT: Girardin, Stephen
; TITLE OF INVENTION: CARD-4 MOLECULES AND USES THEREOF

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; FILE REFERENCE: 07334-371004
; CURRENT APPLICATION NUMBER: US/10/966, 846
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 10/706, 857
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: US 10/352, 381
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 10/154, 485
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 10/027, 881
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258, 724
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-966-846-3

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Alignment Scores:
Pred. No.: 2,89e-21 Length: 2859
Score: 347.00 Matches: 204
Percent Similarity: 38.44% Conservative: 122
Best Local Similarity: 24.06% Mismatches: 321
Query Match: 4.91% Indels: 202
DB: 7 Gaps: 37

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US-10-066-521-6 (1-1344) x US-10-966-846-3 (1-2859)

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Qy      189 ThrValValLeuHisGlyLeuSerGlyIleGlyIleSerAlaLeuValArgArgIleVal 208
Db      589 ACCATCTTCACTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
Qy      209 LeuCySTPAlaGlnGlyGlyLeuTyGlnGlyMetPheSerTyValPhePheLeuPro 228
Db      649 AGCCTCTGGGCGACGGGCGGCTGACGACGAGGGGTC--AAATCTTCTTCACTTTCGC 705
Qy      229 ValArgGluMetGlnArgLeuLeuSerSer-----ValThrGlnPheIleSer 245
Db      706 TGCCTGATGTTCACTGCTTCAAGAGAAAGTGAAGAGGCTGTGTCTGACAGACTGCTTTC 765
Qy      246 ArgGluTrp-----ProAspSerGlnAlaProValThrGluIleMetSerArg 261
Db      766 AAGACTACTGTGATCCAGAGAGGAGAGCCCGAGAGAGGTGTTGCTCTGCTGCGCTTC 825
Qy      262 ProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsn 281
Db      826 CCCACGTGGCCCTCTTCACTTCGATGAGGCTGAGAGAGTGCACCTCGGACTTG----- 879
Qy      282 AspThrIleLeuCysLeuAsp-----TrpAlaGlnLeuGlnProProPheThr 297
Db      880 GACCTGACCCGCGCTGACAGGCTCTGCCCCCTGG--GAGCTGCCACCTCCCTGGTC 936
Qy      298 LeuIleArgSerLeuLeuArgGlyValLeuLeuProGluSerPheLeuIleValThrVal 317
Db      937 TTGCTGGCAACTCTCTCAAGTGAAGCTGTCTCAAGGGGGGCTAGCAAGCTGTCTCAAGCC 996
Qy      318 Arg-----AspValGlyThrGlnLeuLeuLeuSerGlnValValSerProArgTy 334
Db      997 GCGACAGGCAATCAGAGTCCCGCGCAAGTTCCTGCGAGAAAGGTG----- 1041
Qy      335 LeuLeuValArgGlyIleSerGlyIleGlnGlnArgIleHisLeu----- 348
Db      1042 ---CTTCTCGGGGCTTCTCCCGCAGC-----CACCTGCGCGGCTATGCCAGAG 1089
Qy      349 ---LeuLeuGluArgGlyIleGlyIleHisGlnLeuThrGlnGlyLeuArgAlaIleMet 367
Db      1090 ATGTTCCCGGAGCGGGGCTGAGAGACCGGCTGTGAGCCAG-----CTGGAG 1137
Qy      368 AsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValAlaGlySerLeuIleCysVal 387

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Db 1138 GCCAACCCCAACCTTCAGCCTGTGCTGTGCGCC-----CTCTTCTGTGCTGG 1185  
 QY 388 AAlaLeu-----GlnLeuGln 392  
 Db 1186 ATCATCTTCGCGGTCTTCAGCACTTCGCTGCTTTGAAGGCTTCACCAAGCTGCCCC 1245  
 QY 393 AspValValGlyGlnSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAla 412  
 Db 1246 GACTGC-----ACGATGACCTTCAGATGATGCTTCCTGCTG 1281  
 QY 413 PheVal-----PheHisGlnLeuThrProArgGlyValAlaArgArgCysLeuAsn 429  
 Db 1282 GTCACCTGAGGTCCATCTGAGACAGAGATGACGCCAGCAGCTGTGGACCG-----AAC 1335  
 QY 430 LeuGlnGlu-----ArgValValLeuLysArgPheCysArg 441  
 Db 1336 ACAAGCAGCCCACTGAGAGACCTTCACGCGCGGAGCACTGTGCTGCGGGGAG 1395  
 QY 442 MetAlaValGlnGlyValThrAsnArgLysSerValPheAspGlyAspAspLeuMetVal 461  
 Db 1396 GTGGCCCAAGCGGAGCATGAGAAAGAGCTTTGTCTTCAACCAAGAGAGGTGACAGCC 1455  
 QY 462 GlnGlyLeuGlyGlnSerGln-----LeuArgAlaLeuPheHisMetAsn 476  
 Db 1456 TCCGGGCTGCGAGAGACATGACAGCTGCGCTTCCTGCGGCTTGGCGAGCTGGC 1515  
 QY 477 IleLeuLeuProAspSerHisCysGlnGlnLysThrPhePheHisLeuSerLeuGln 496  
 Db 1516 -----CCCGGGGGGTGAC--CAGCAGCTTATGAGATTTCACCTTCACCTTCAG 1563  
 QY 497 AspPheCysAlaAlaLeuLysThrValValLeuGln----- 507  
 Db 1564 GCCTTCTTTACAGCTTCTTCTGCTGTGAGACAGAGGAGGACACTCAGAGCTGCTC 1623  
 QY 508 -----GlyLeuGlnIle-GluProAlaLeu----- 515  
 Db 1624 AGGTTCTTCAGAGATGATGATCCCTTCGCGGGGAGCAGCAAGTCTCTATCTCC 1683  
 QY 516 -----CysProLeuLysThrValGlnLysThrLysArgSerMetGluLe 529  
 Db 1684 TTCTCTCCGTTCCAGCTGCTGACAGGAGAGTGTGCGCGGAGAGACCTTTCAAAAC 1743  
 QY 529 LysGlnAlaGlyPheHisIleHisSerLeuTrpMetLysArgPheLeuPheGlyLeuVal 549  
 Db 1744 -AAGAA-----CACTTCAGATTCAACAACCTTCTGCGGGGCTGT 1787  
 QY 549 LysGlnAspValArgArgProLeuGlnValLeuLeuGlyCysProValProLeuGlyVal 569  
 Db 1788 GTCCAAAGCCAAACAGAAACCTCTGCGGCACTGTGTCGCCGCG--GCAAGCCTCAGAGAG 1844  
 QY 569 LysGlnLysLeuLeuHisIleThrValSerLeuLeuGlyGlnGlnProAsn-----AlaThr 587  
 Db 1845 AAAGCCGAAAGCCCTG--TGGGCAACCTGTTTCCAGCTGCGGGGCTAAGAAAG 1901  
 QY 587 rThrProGlyAspThrLeuAspAlaPheHis----- 597  
 Db 1902 CCGAGCCCGGTTGAGGTTCAGAAAGCTTCAACAGATGAGGCCATGCCCCAGTTCACTG 1961  
 QY 598 -----CysLeuPheGlnThrGlnAspLysGlnPheValArgLeuAlaLeuAsn 614  
 Db 1962 GATGCTGCGCTGCTGATCTGACAGACAGAGCAGAGGTGGGCGGCGGCGGCGG 2021  
 QY 614 rPheGlnGlnValThrLeuProIleAsnGln-----AsnLeuAspLeuIleAl 630  
 Db 2022 CATCTGCGCAACTCACTCAAGCTGACTTACTGCAAGCCCTGCTGCGCCAGCTGACGCG 2081  
 QY 630 AspSerPheCysLeuGlnHisCysProLysThrLeuArgLysIleArgValAspValLysG 650  
 Db 2082 CCTCTCTTGGCTGCTGATCACTTCCCC-----AAAGGCGTGGCCCTTAAGCAAGCA 2135  
 QY 650 yLlePheProArgAspGlnSerAlaGlnAlaCysProValValProLeuTrpMetLysG 670  
 Db 2136 CAACAATCTCAACGATCAAGCGGCTGCGG-----GAGCTGAGCTTGTCAAGCCGC- 2187

QY 670 pLysThrLeuIleGlnGlnIntrGlnAspPheCysSerMetLeuGlyThrHisProH 690  
 Db 2187 ----- 2187  
 QY 690 sLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnValAlaMetLysThrLeu 710  
 Db 2188 -CTCACTGTTCTCACTGCTGACCGCTTAACAGATCACTGAGCGTGGGTAAAGGTCTAG 2246  
 QY 710 sAlaLysLeuArgHisProThrCysLysIleGlnThr-----LeuMetPheArgAsnAla 729  
 Db 2247 CGAAGGCTG-----ACCAATACAAATTTGACCTTATTTGGTTTACAAACCA 2300  
 QY 729 nIleThrPro-----GlyValGlnHisLeuThrArgIleValMetAlaAsnArgAsnLeu 748  
 Db 2301 GATCAACCGATGTGGAGCCAGGATACGTACCAAAATCTGTGATGAAATGCAAAAGCTCAC 2360  
 QY 748 gSerLeuAsnLeuGlyGlyThrHisLeuLysGlnGlnAspValArgMetAlaCysGlnAl 768  
 Db 2361 GCATCTTAACTGGGAAACAAATTAACAAGTGAAGAGGAGAAATCTCCGCTGCG 2420  
 QY 768 sLeuLysHisProLysCysLeuLeuGlnSerLeuArgLeuAspCysGlyLeuThrHis 788  
 Db 2421 TGTGAAGAACAGCAA----- 2436  
 QY 788 sAlaCysTyLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeu 808  
 Db 2437 -----TCAATCTGAGGTTGG 2453  
 QY 808 rLeuAlaGlyAsnLysValThrAspGlnGlyAlaMetProLeuSerAspAlaLeuArgVal 828  
 Db 2454 GATGTGGGGCAATCAAGTTGGGATGAAAGAGCAAAAGCCTTGCGAGAGCTTCGCG-- 2511  
 QY 828 LysGlnCysAlaLeuGlnLysLeuIleLeuGlnAspCysGlyTlIleThrAlaThrGlyC 848  
 Db 2512 -AACACCCAGCTTGACCACTGAGTCTTGCGTCCAAAGGATCTCCACAGAGAGG 2570  
 QY 848 sGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAs 868  
 Db 2571 AAAGAGCTTGCAGAGGCGCTTCGACAGCAACAGTCTCTGAATACTGTGCTGACCA 2630  
 QY 868 nAsnSerLeuGlyAsnGlnGlyValaLeuLeuLeuCysArgSerMetArgLeuProHisC 888  
 Db 2631 AAATGAATCAAGATGAAATGTCAGAGAGTTGGCAAAATGTGAAAGTCC--AACCA 2687  
 QY 888 sSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLe 908  
 Db 2688 GAGCTTAAGCAATTATGCTTATCCGAATCAGATCAAGCTTAAGGGAGCTGCCAGCT 2747  
 QY 908 uAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProVa 928  
 Db 2748 GCGAGATGCGTTTACAGAGCAACATGCGCATTAACAGAGATTGCTTAATGAAGAACTGAT 2807  
 QY 928 lGluAspAsnGlyValLysLeu 935  
 Db 2808 AAAACAGAGAGGCCAAAGTTC 2829  
 RESULT 7  
 US-11-147-047-23  
 ; Sequence 23, Application US/11147047  
 ; Publication No. US2005026068A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agarwal, Pankaj  
 ; APPLICANT: Rizvi, Safia K.  
 ; APPLICANT: Murdock, Paul R.  
 ; APPLICANT: Smith, Randall F.  
 ; APPLICANT: Xiang, Zhaoyang  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP50016  
 ; CURRENT APPLICATION NUMBER: US/11/147, 047  
 ; PRIOR FILING DATE: 2005-06-07  
 ; PRIOR APPLICATION NUMBER: US/10/221, 097  
 ; PRIOR FILING DATE: 2002-09-06

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PRIOR APPLICATION NUMBER: PCT/US01/07143
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/236,874
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/188,916
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/237,846
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 3213
TYPE: DNA
ORGANISM: Homo sapiens
US-11-147-047-23

Alignment Scores:
Pred. No.: 6,64e-15 Length: 3213
Score: 280.00 Matches: 233
Percent Similarity: 37.39% Conservative: 157
Best Local Similarity: 22.34% Mismatches: 348
Query Match: 3.96% Indels: 308
DB: Gaps: 51

US-10-066-521-6 (1-1344) x US-11-147-047-23 (1-3213)
QY 191 ValLeuHISgLYLysSerGIYleGIYsSerAlaLeuAlaArgArgIleValLeuCYs 210
DB 634 ATCATTTGAAGGGGAATCTGGCAAGGCAAGTCCACTGCTGCAAGCGAATGCCATGCTC 693
QY 211 ThrAlaGlnGlyGlyLeuTYrGln---GlyMetPheSerTYrValPhePheLeuProAla 229
DB 694 TGGGCTCTCCGAAGGTGCAAGGCTCTGACCAAGTTCAATTCGTTCTTCTCCGCTC 753
QY 230 ArgGluMetGlnArgLYleGlyLeuSerSerValThrGluPheIleSerArgGluThrPro 249
DB 754 AGCAGGGGCCAG---GCTGACCTTTTGAACCTCTGTGATCACTCTG 801
QY 250 Asp-----SerGlnAlaProValThrGluIleMetSerArgProGlu 263
DB 802 GATTAACCTGGCACATCAGAGACATTCATGCGATGCTGCAAGCTGCGCAG 861
QY 264 ArgLeuLeuPheIleIleAspGlyPheAspPheLeuGlySerValLeuAsnAspThr 283
DB 862 AGGGTTCTTCTCTTGATGGCTACATGATTC-----AAGCC 903
QY 284 LysLeuCYsLYsAspThrAlaGluLYsGlnProPheThrLeuIleArgSerLeu 303
DB 904 CAGAACTGCCAGAA-----ATCGAAGCCTGATA 933
QY 304 ArgLYsValLeuLeuProGluSerPheLeuIleValThr----- 316
DB 934 AAGGAACCAACCGCTTCAAGAACATGCTCATCGCACCACTACCACTGAGTGCCTGAG 993
QY 317 ---ValArgAspValGlyThrGluLYsLeuSerGlnValValSerProArgTYrLeu 335
DB 994 CACATCGCGAGTTTGTC---CTGACTGCTGAGTGGGGAATATGACAGAAAC 1047
QY 336 LeuValArgGlyIleSerGlyGluGlnArgIleIleLeuLeuGluArgGlyIleGly 355
DB 1048 AGCCGCCAGGCTCTATCCGAAAGTGTGATCAAGACGCTTGGAGGCTTGTC 1107
QY 356 GluHISglnLYsThrGlnGlyLeuArgAlaIleMetAsnAspArgGluLeuAspGln 375
DB 1108 CAATTCAGAAATCAGAGTGTGCTTGAAGATCTCATG----- 1143
QY 376 CysGlnValProAlaValGlySerLeuIleCYsValAlaLeuGlnAspValVal 395
DB 1144 ---AAGACCCCTCTTGTGTGCTCATCTGT---GCATCCAAATG----- 1185
QY 396 GlyLeuSerValAlaProPheAsnGlnThrLeuThrGlyLeuHISAlaAlaPheValPhe 415

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DB 1186 GGTGAAGTGAAGTTCCACTCTCACACAAACAGCTGTTCAT-----ACCTTC 1236
QY 416 HisGlnLeuThrProAlaGlyValValArgArgCYsLeuAsnLeuGluGluArgValVal 435
DB 1237 TATATCTCG-----TTGATACGAAAAACAAACCAATTAAGGTGTGCT 1284
QY 436 LeuLYsArgPheCYsArg-----MetAlaValGluGlyValThr 448
DB 1285 GCAAGTGACTTCAATTCGAGGCTGAGACCACTGAGAGCCTGAGCTGAGAGGTGTTC 1344
QY 449 AsnArgLYsSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGlySerGlu 468
DB 1345 TCCCAAGATTGATTGCAACTGACAGAT-----GTGTCCAGCTGCAATGAG----- 1392
QY 469 LeuArgAlaLeuPheHISMetAsnIleLeuLeuProAspSerHISCYsGluGluTYr--- 487
DB 1393 ---GATGCTCTGTGCAACTGGGCTCTCTGTAAATATACA 1431
QY 488 ---TYrThrPhePheHISLeuSerLeuGlnAspPheCYsAla 500
DB 1432 GCTCAAGTTCACAGCCAAATATTAATTTCTTCAAGATCATTCAGAGATACAGCA 1491
QY 501 Ala-----LeuTYrTYrValLeuGluGlyLeuGluIleGluProAlaLeuCYsProLeu 518
DB 1492 GAGCAAGACTCACAGATTATGACGCTCATGACGACAG----- 1533
QY 519 TYrValGluLYsThrLYsArgSerMetGluLeuLYsGlnAlaGlyPheHIS----- 535
DB 1534 ---GAGTGACCAAGGGAATGTGTTCTTGCAGAAAT---GGTTTCATTTGCGACAT 1586
QY 536 ---IleHis---SerLeuTrpMetLYsArgPheLeuPheGlyLeuValSerGluAspValArg 554
DB 1587 TACATTCATTTATGACAGCTGCTCCGCTACACCGTGCGGCATGTGAGAACACAG 1646
QY 554 GArgProLeuGluValLeuLeu-----GlyCYsProValProLeuGlyVal 569
DB 1647 GCGTTATGAAAGCACTCGCAGAGTATCAACAGCGCTGCTTCCGACATTTCCAT 1706
QY 569 LYsGlnLYsLeuLeuHISTrpValSerLeuGluGlyGlnGlnProAsnAlaThrPr 589
DB 1707 CGCAAGAGGCTCTC---TGAAGACAGAAATCTTTGCAAAAGTGAACCACTGCA 1763
QY 589 GGLYsAspThrLeuAspAlaPheHISCYsLeuPheGluThrGlnAspLYsGluPheValArg 609
DB 1764 GCAAGAAATTTGAAAGCCATAAACATC-----AATTCCTTGTGA 1805
QY 609 GLeuAlaLeuAsnSerPheGlnGlu---ValTrp-----LeuProIleAsnGlnLeuVal 627
DB 1806 GTGTGACATCATTTATATCAAGAGATACATCCAAATCAGCCCTGAGCCAAAGATTGA 1865
QY 627 sPheIleIleAspSerPheCYsLeuGlnHISCYsProTYrLeuArgLYsValLeuArgVal 647
DB 1866 AGCTT-----TCTTTCAAGGA-----AAAGCTTATATAT 1895
QY 647 sPValLYsGlyIlePheProArgAsp-----GluSerAlaGluAlaCYsProValVal- 664
DB 1896 CAATCAGGAAACATCCCGATTAATTGACTTCTTGAACATTTGGCCAAATGTGCG 1955
QY 665 -----ProLeuTrpMetArgAspLYsT 672
DB 1956 AAGTCCCTGACATTCAATTAATGCACTTTTATGAGGAGACCTATGCTCATGAGAA 2015
QY 672 HTrpIleGluGluGln---TrpGluAspPheCYsSerMetLeuGlyThrHISProHISLeu 691
DB 2016 GAGCTGCAAGAACACAGGTG-----AATCCAT--- 2045
QY 692 ArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLYsThrLeuCYsAla 711
DB 2046 ---GGAAGAGGCCCAAGAAACTACATTC 2072
QY 712 LysLeuArgHISProThrCYsLYsIleGlnThrLeuMetPheArgAsnAlaGlnIleThr 731

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Db 2073 CAG-----CAGGGCTGTATCTT---GTTCTTCAACGTGAA 2105
Qy 732 ProGlyValGlnHisLeuThrArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsn 751
Db 2106 GCGAGAAATTGAGA-CTCTGAGGTC-ACACTC-----CGGATTTGACGAAGTTGAAT 2157
Qy 752 LeuGlyValThrHisLeuArgValAspValArgMetAlaCysGluAlaLeuValHis 771
Db 2158 -----MACGAGATATCGATATCTGGGGAATAATTCAGCTCT 2196
Qy 772 ProLysCysLeuLeuGlnSerLeuArgLeuAsp-----CysCysGlyLeuThrHis 788
Db 2197 -----GCCACAGCCTCAGCGCTCAATAAGATATGCTGGTGTGGCTGGA 2244
Qy 789 AlaCysThrLeuLysIleSerGlnIleLeuThrHisProSerLeuLysSerLeuSer 808
Db 2245 AGC-----CTCAGTTGGTCTCAGCAGCTGTGAAGACATTATTTCTCTATG 2292
Qy 809 LeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVal 828
Db 2293 GTGGAAGCCAGTCCCTCACC-----ATGAGAGATGAGAGGACATC 2334
Qy 829 SerGlnCysAla---LeuGlnLysLeuIleLeuGluAspCys-----841
Db 2335 ACATCTGTACAACAACTGAAACCTTGATATCATGACCTACAGAAATCAACGGCTCCG 2394
Qy 842 ---GlyLeuThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db 2395 GGTGGTCTGACT-----GACAGCTTGGGTAACTTGAAAGAC 2430
Qy 861 LeuThrHisLeuCysLeuSerAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCys 880
Db 2431 CTTCACAAAGCTCATATGATGATACATAAAGATGAAGAAGTGTATTAACATGAGT 2490
Qy 881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetCysLeuAsnGlnCysHisLeu 900
Db 2491 GAAGGCTGAAA-----AACCTGAAGAGATGTTGTTATTTTCAT- 2529
Qy 901 AspThrArgLeuGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920
Db 2530 -----TTGACCCAC 2538
Qy 921 LeuSerLeuSerMetAsnProValGluAsp-----AsnGlyValLysLeuLeuCysGlu 938
Db 2539 TTGTCT-----GACATGAGAGGGAATGATCATATGATCAG 2577
Qy 939 ValMetArgGluProSerCysHisLeuGlnAspLeuLeuValLysCysHisLeuThr 958
Db 2578 TCTCTGTCAAGTGAACCTGTGACCTTGAGAAATTCATATTAATCTCTGCTGTGTCT 2637
Qy 959 AlaAlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978
Db 2638 GCAAAATGCAAGTGAATCTTACGTCAAGATCTTCAATTTGGTCAAACTGAGCATTTCTT 2697
Qy 979 AspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlnGlyLeuLys 998
Db 2698 GATTATACAGAAATTTACTGTGAAGAAAGATGAAGAGTCTTCAATGAATCATGATGAC 2757
Qy 999 GlnLysAsnSerVal-----1003
Db 2758 AGATGAACGTGTGAAGACAGCTCACCGCATGTGCTGCCCTGGGCTGTGACGTGCAA 2817
Qy 1004 -----LeuThrArgLeuGly 1008
Db 2818 GGCAGCCTGAGCAGCCTGTGGAACATTGGAGGAGGTCCCAACACTGTCGAACCTTGGG 2877
Qy 1009 LeuValAlaCysGlyLeuThrSerAspCysCysGlyAlaLeuSerLeuAlaLeuSerCys 1028
Db 2878 TTGAAAAAATCGAAGATCTACAGATACAGAGATTTGAATTTTATAGTGCATTTTGGGAAG 2937
Qy 1029 Asn-----ArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db 2938 AACCTCTGAAGAAATCTTCAGCAGTGAATTTGGCGGGAATCTGTGACAGCATGATGGA 2997

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Qy 1047 MetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleLeuGlyLeu 1066
Db 2998 TGGCTTGCCCTTCAATGGGTGATTT-----GAGAAATCTTAAGCAATTAAGTCTT 3045
Qy 1067 TrpLysTrpGlnTrp-----ProValGlnIleArgLysLeu-----1078
Db 3046 TTTGACTTTAGTACTAAGAAATTTCTACCTGATCCAGCATTAATGAGAAACCTTAGCCAA 3105
Qy 1079 -----LeuGlnGluValGlnLeuLeuLysProArgValValIle 1091
Db 3106 GTGTATCAAGTAACTTTTGTGCAAGAAAGTAAAGCTGTCT- 3147
Qy 1092 AspGlySerThrHisSerPheAspGluAspAspArgHisLysIleGlyLeuThrPheArg 1111
Db 3148 -----GGGTGG---CAATTTGATGATGATGATCTGATCTATTAACAGGTGCTTTAAA 3198
Qy 1112 Leu 1112
Db 3199 CTA 3201

RESULT 8
US-11-145-631-3
; Sequence 3, Application US/11145631
; Publication No. US20060003409A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OR INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREK
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/11/145,631
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-145-631-3

Alignment Scores:
Pred. No.: 1,46e-14 Length: 3072
Score: 276.00 Matches: 232
Percent Similarity: 37.30% Conservative: 157
Best Local Similarity: 22.24% Mismatches: 349
Query Match: 3.50% Indels: 308
DB: 8 Gaps: 51

US-10-066-521-6 (1-1344) x US-11-145-631-3 (1-3072)
Qy 191 ValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgIleValLeuCys 210
Db 496 ATCATTAAGGGAATGTGGCAAAAGCAAGTCACTGCTGCAAGCATTTGCCATCTC 555
Qy 211 TrpAlaGlnGlyLeuTrpGln---GlyMetPheSerTrpValPhePheLeuProVal 229
Db 556 TGGGGCTCCGAAAGTCAAGGCTGTGACCAAGTTCMAATTGCTTCCTCCGCTC 615
Qy 230 ArgGluMetGlnArgLysLysGlnSerSerValThrGluPheIleSerArgGluTrpPro 249
Db 616 AGCAGGGCCAG-----GGTGAACCTTTTAAACCCCTCTGTATCAACTCTTG 663
Qy 250 Asp-----SerGlnAlaProValThrGluLysLeuMetSerArgProGlu 263
Db 664 GATTAATCTGCAACAATCAGAAAGACATTCATGACCATGCGCTGGAAGCTGGCGGAG 723
Qy 264 ArgLeuLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThr 283

```

Db 724 AGGGTTCTTTCTTGTGATGGTACATGAATTC-----AAGCCC 765  
 Qy 284 LysLeuCyLeuSerTrpAlaGluValGlnProProthLeuLeuLeuSerLeuLeu 303  
 Db 766 CAGAACTGCCAGAA-----ATCGAAGCCCTGATA 795  
 Qy 304 ArgLysValLeuLeuProGlnSerPheLeuLeuLeuLeuLeuLeu 316  
 Db 796 AAGGAAACACCGCTTCAGAAATGCTATCTGACACCTACCTAGCTGCTGAG 855  
 Qy 317 ---ValArgAspValGlyThrGluValLeuLysSerGluValValSerProArgTrpLeu 335  
 Db 856 CACATACGAGCTTGGTGGC-----CTGACTCTGAGGTGGGATATGACAGAAC 909  
 Qy 336 LeuValArgGlyLeuSerGlyGluGlnArgLeuLeuLeuLeuGluArgGlyLeuGly 355  
 Db 910 AGCGCCAGGCTCATCCAGAAAGTGTATCAAGAGCTTGTGAAGCTTGTGTC 969  
 Qy 356 GluHisGlnLysThrGlnGlyLeuArgAlaLeuMetAsnAsnArgLysLeuLeuAspGln 375  
 Db 970 CAATTCAGAAATCAGAGCTTGAAGATTCATG----- 1005  
 Qy 376 CysGlnValProAlaValGlySerLeuLeuCysValAlaLeuGlnLeuGlnAspValVal 395  
 Db 1006 ---AAGACCCCTCTTTGTGTGTCATCTGT---GCAATCCAGATG----- 1047  
 Qy 396 GlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPhe 415  
 Db 1048 GGTAAAGTGGTTCACCTCCACACAAACAGCTGTTCAT-----ACCTTC 1098  
 Qy 416 HisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGluGluArgValVal 435  
 Db 1099 TATATGTG-----TTGATTCAGAAACAAACAAACATTAAGGTGGCT 1146  
 Qy 436 LeuValArgPheCysArg-----MetAlaValGluGlyValTrp 448  
 Db 1147 GCATGACTTCATTCGAGCTGGACCTGGACCATGTCGAGACCTAGCTCGAGGGGTGTC 1206  
 Qy 449 AsnArgLysSerValPheAspGlyAspArgLeuMetCysAlaGlnGlyLeuGlyLysSerGlu 468  
 Db 1207 TCCCAAGATTGATTCGAACTGCAGAT-----GTGTCAAGCTGTAATGAG----- 1254  
 Qy 469 LeuArgAlaLeuPheHisMetAsnLeuLeuLeuProAspSerHisCysGluGluTrp--- 487  
 Db 1255 ---GATGTCTGCTGACAACTGGGCTCTCTGTAATATATCA 1293  
 Qy 488 ---TyrThrPheHisLeuSerLeuGlnAspPheCysAla 500  
 Db 1294 GCTCAAGCTTCAGGCCAAATATTAATCTTTCACAGTCACTTCACAGAGTACAGCA 1353  
 Qy 501 Ala-----LeuTyrTyrValLeuGluGlyLeuGluLeuGluProAlaLeuCysProLeu 518  
 Db 1354 GACGAAAGACTCAGCAGATTATGACTCTCATGAGCCAG----- 1395  
 Qy 519 TyrValGlyLysThrLysArgSerMetCysLeuLysGlnAlaGlyPheHis----- 535  
 Db 1396 ---GAGGTGACCAAGGAAATGTTACTTGACAAAT---GGTTTCATTTCCGACAT 1448  
 Qy 536 ---HisSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValAla 554  
 Db 1449 TACATCCATTATGACAGCTGCTCCGCTACACCTGTGGTCATGTGGAAGCCAG 1508  
 Qy 554 ArgTrpLeuGluValLeuLeu-----GlyCysProValProLeuGlyVal 569  
 Db 1509 GAGCTGTATGAAGCTCGACAGATGATCAACAGCGCTGCTTCGAGCTTCCAT 1568  
 Qy 569 LysGlnLysLeuLeuHisTrpValSerLeuLeuGlyGlnGlnProAlaAlaThrTrp 589  
 Db 1569 GCGCAAGGCGCTTC---TGAGACAGAAATCTTTCGAAAGTGAAGAAACACAG 1625  
 Qy 589 GglLysArgThrLeuSerAlaPheHisCysLeuPheGlnThrGlnAspLysGluPheValAla 609  
 Db 1626 GAAAGAAATTCGAAAGCCATTAACATC-----AATTCCTTTGTGGA 1667

Qy 609 GluAlaLeuAsnSerPheGlnGluValTrp-----LeuProLeuAsnGlnAsnLeu 627  
 Db 1668 GTGGCATCATCTTATATCAAGAGTACATCCAAATGAGCCCTGAGCCAGAAATTTGA 1727  
 Qy 627 sPheLeuLeuAsnSerPheCysLeuGlnHisCysProTyrLeuArgLysLeuArgVal 647  
 Db 1728 AGCTT-----TCTTCAAGGTA-----AAAGCTTATATAT 1757  
 Qy 647 sPValLysGlyLeuPheProArgAsp-----GlnSerAlaGluAlaCysProValVal 664  
 Db 1758 CAACTCAGGAAACATCCCGATTAATTATTAAGTCTTTGAAACATTTGCCAATTTGTC 1817  
 Qy 665 -----ProLeuTrpMetArgAspLysTrp 672  
 Db 1818 AAGTCTGTGACTTCAATTAATGACCTTTATGGGGAGCTATGCTTCATGGGAAA 1877  
 Qy 672 hTrpLeuLeuGluGlnGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHisLeu 691  
 Db 1878 GGTGCAAGAACACAGCTG-----AATCCCAT--- 1907  
 Qy 692 ArgGlnLeuAspLeuGlySerSerLeuLeuThrGluArgAlaMetLysThrLeuCysAla 711  
 Db 1908 -----GAAAGAGGCCCAAGAACTTCATTC 1934  
 Qy 712 LysLeuArgHisProThrCysLysLeuGlnThrLeuMetPheArgAsnAlaGlnLeuThr 731  
 Db 1935 CAG-----CAGGCTGTATCTTT---GTCTTCAACTGGA 1967  
 Qy 732 ProGlyValGlnHisLeuTrpArgLeuValMetAlaAsnArgLeuAspSerLeuAsn 751  
 Db 1968 GCAGAAATTCAGAG-CTCTGAGGTC-ACATC-----CGGATTCAGCAAGTGAAT 2019  
 Qy 752 LeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLysHis 771  
 Db 2020 ---AAGCAAGATATACATATCTGGGAAATATTCAGCTCT 2058  
 Qy 772 ProLysCysLeuLeuGlnSerLeuArgLeuAsp-----CysCysGlyLeuThrHis 788  
 Db 2059 ---GCCAAGCTCAGGCTGCAATTAAGAGATGCTGCTGCTGCTGCA 2106  
 Qy 789 AlaCysTyrLeuLysHisSerGlnLeuLeuThrHisSerProSerLeuLysSerLeuSer 808  
 Db 2107 AGC-----CTCAGTTGTGCTCAGCACCTGTAAGACATTAATTTCTCTCAWG 2154  
 Qy 809 LeuAlaGlyAsnLysValThrAspGlnGlyAlaMetProLeuSerAspAlaLeuArgVal 828  
 Db 2155 GTGAAAGCCAGTCCCTCAC-----ATAGAAGATGAGAGCACATC 2196  
 Qy 829 SerGlnCysAla-----LeuGlnLysLeuLeuLeuGluAspCys----- 841  
 Db 2197 ACATCTGTAAACAACTGAAACCTTAGATTAATCACTCAACAAATCAACGCTGCG 2256  
 Qy 842 ---GlyLeuThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860  
 Db 2257 GGTGTGACT-----GACACTTGCGTAATTAAGAAC 2292  
 Qy 861 LeuThrHisLeuCysLeuSerAsnAsnSerLeuGluAsnGluGlyValAsnLeuLeuCys 880  
 Db 2293 CTTCAAAGCTCAATAGATGATTAAGATGAAGATGAAGATGCTATTAATTAACCT 2352  
 Qy 881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900  
 Db 2353 GAAAGCTGAA-----AAGCTTAAGATGTATTATTTCAAT----- 2391  
 Qy 901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920  
 Db 2392 -----TTGACCCAC 2400  
 Qy 921 LeuSerLeuSerMetAsnProValGluAsp-----AsnGlyValLysLeuLeuCysGlu 938  
 Db 2401 TTGTCT-----GACATTTGAGAGGAAATGATTAATCACTGTCAAG 2439



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QY 939 ValMetArgGluProSerCysHisLeuGlnAspLeuGluValLysCysHisLeuThr 958
Db 2440 TCCTGTGCAAGTAAACCCCTGTGACCTTGAAGAAATTCATTATGCTCTCTCTGCTTCT 2499
QY 959 AlAlaCysCysGlnSerLeuSerCysValLLeSerArgSerArgHisLeuLysSerLeu 978
Db 2500 GCAATGTGACGTAATAATCTAGCTAGCAATCTTCACAATTTGGTCAACAGTACGATCTT 2559
QY 979 AspLeuThrAspMetAlaLeuGlyAspGlyGlyValAlaLeuCysGlyGlyLeuLys 998
Db 2560 GATTTATCAGAAAATTTACTGGAAGAAATGAAATGAAAGCTCTTCATGAACTGATCAG 2619
QY 999 GlnLysAsnSerVal----- 1003
Db 2620 AGCATGACCTGCTGAAGAACAGCTCACCGCACTGATGCTGCGGCTGAGACGTGCA 2679
QY 1004 -----LeuThrArgLeuGly 1008
Db 2680 GGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGAGAGTCCCAACATCTGTCACAGCTTGG 2739
QY 1009 LeuLysAlaCysGlyLeuThrSerAspCysGlyLysLeuLysSerLeuAlaLeuSerCys 1028
Db 2740 TTGAAGAACTGAGAGACTCACAGATACAGAGATTGAATTTAGTGCAATTTTGGAAAG 2799
QY 1029 Asn-----ArgHisLeuThrSerLeuAsnLeuValGlnAsnAspSerProLysGly 1046
Db 2800 AACCTCTGAAAAAATCTCCAGCAGATTGAATTTGGCGGAAATCGTGTGACAGATGGA 2859
QY 1047 MetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnLeuGlyLeu 1066
Db 2860 TGGCTTCCTTCATGAGGTGATTT-----GAGAACTCTTAAGCAATTAGTGT 2907
QY 1067 TrpLysThrGlnLys-----ProValGlnLeuGlyLeu----- 1078
Db 2908 TTGACTTACTGACTAAAGATTCTACCTGATCCAGCATTTAGTCAGAAACTTAGCCAA 2967
QY 1079 -----LeuGlnGluValGlnLeuLysProArgValAlaLeu 1091
Db 2968 GTGTTATCCAGTTAACTTTTCTGCAAGAAAGCTAGGCTTGT----- 3009
QY 1092 AspGlySerTrpHisSerPheAspGlnAspAspArgHisLysLysIleGlyLeuThrPheArg 1111
Db 3010 -----GGGTGG---CAATTTGATGATGATGATCTCAGTGTATTATACAGGTGCTTTTAA 3060
QY 1112 Leu 1112
Db 3061 CTA 3063

RESULT 9
US-11-136-527-4003
; Sequence 4003, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probes Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4003
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4003

Alignment Scores:
Pred. No.: 1,51e-14 Length: 3133
Score: 276.00 Matches: 232
Percent Similarity: 37.30% Conservative: 157

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Best Local Similarity: 22.24% Mismatches: 349
Query Match: 3.90% Indels: 308
Db: 8 Gaps: 51

US-10-066-521-6 (1-1344) x US-11-136-527-4003 (1-3133)
QY 191 ValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgIleValLeuCys 210
Db 531 ATCATTTGAAGGGGAATCTGGCCAAAGGCAAGATTCACCTGTGTCGAGCGCATTCAGCTC 590
QY 211 TrpAlaGlnGlyLeuLysGln---GlyMetPheSerTrpAlaPhePheLeuProVal 229
Db 591 TGGGGCTCCGGAAAGTCAGAGGCTTGACCAAGTGTCAAAATTCGTCCTTCCCTCGCTG 650
QY 230 ArgLysMetGlnArgLysLysGlnSerValThrGlnPheIleSerArgGluTrpPro 249
Db 651 AGCAGGGCCAG-----GGTGACCTTTTGAACCTCTGTATCACTCCTG 698
QY 250 Asp-----SerGlnAlaProValThrGlnLysMetSerArgProGlu 263
Db 699 GATATACCTGGCAATCAGAGAGAGACATTCATGAGCCATGCTGCTGAAGCTGCGGAG 758
QY 264 ArgLeuLeuPheLeuIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThr 283
Db 759 AGGGTCTTTTCTTCTTGTATGACTCAATGAATTC-----AGCCC 800
QY 284 LysLeuCysLysAspTrpAlaGluLysGlnProProPheThrLeuLeuArgSerLeuLeu 303
Db 801 CAGAACTGCCCAAA-----ATCGAAGCCCTGATA 850
QY 304 ArgLysValLeuLeuProGlnSerPheLeuIleValThr----- 316
Db 831 AAGAAACCAACCGCTTCAAGAAACATGTCATGTCACCACTACCACTGAGTGCCTGAGG 890
QY 317 ---ValArgAspValGlyThrGluLysLeuLysSerGlnValAlaSerProArgTrpLeu 335
Db 891 CACATACGAGGATTTGGTGTCC-----CTGACTGTGAGGTGGGGGATATACAGAAAG 944
QY 336 LeuValArgGlyLysSerGlyGlnArgIleHisLeuLeuLeuGlnArgGlyIleGly 355
Db 945 AGCGCCACAGGCTCTCATCCAGAAAGTCGATCAAGAGGCTTGCTGAAGGCTTGCTC 1004
QY 356 GlnHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGln 375
Db 1005 CAATTCAGAAATCCAGGTGCTTGAGGAATCTCATG----- 1040
QY 376 CysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeuGlnAspValVal 395
Db 1041 ---AAGACCCCTCTCTTTGTGTCATCATTTGT---GCAATCCAGATG----- 1082
QY 396 GlyLysSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPhe 415
Db 1083 GGTGAAGTGAAGTTCACCTCTCACACAAACAAAGCTGTTCAT-----ACCTTC 1133
QY 416 HisGlnLeuThrProArgGlyValArgArgCysLeuAsnLeuGlnGluArgValVal 435
Db 1134 TATGATCTG-----TTGATACAGAAAAACAAACAAACATAAAGGTGGCT 1181
QY 436 LeuLysArgPheCysArg-----MetAlaValGluGlyValTrp 448
Db 1182 GCAAGTACTTCAATTCGAGCCTGAGACCACTGAGAGACCTAGCTCGAGGGGTGTTC 1241
QY 449 AsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGlu 468
Db 1242 TCCCAACAAGTTGATTTGCAAGTCAGAGAT-----GTTCAGAGCGGAATGAG----- 1289
QY 469 LeuArgAlaLeuPheHisMetAsnLLeuLeuProAspSerHisCysGlyGluGlyTrp--- 487
Db 1290 -----GATGTCCTGCTGACCAACTGGGCTCCTGTGAATATATACA 1328
QY 488 -----TyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
Db 1329 GCTCAAGGTTCAAGCCAAAGTAAATTTCTTTCACAAAGTCATTTCCAGAGATACAGCA 1388

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Qy 501 Ala-----LeuTyrValLeuGluGluLeuGluProAlaLeuCyProLeu 518
Db 1389 GAGCAAGACCTCAGACGTTATTTGACCTGCATAGACCAAG----- 1430
Qy 519 TyrValGluYbThrIleArgSerMetGluLeuYbGlnAlaGlyPheHis----- 535
Db 1431 -----GAGTGACCAAGGAGAAATGCTTACCTGCAGAAAAT-GGTTTCATTGGGACAT 1483
Qy 536 ---IleHis-SerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGluAspValAr 554
Db 1484 TACATTCACCTTATAGACGCTGCTCCGGTACACCTGTGGTCATCTGGAGAACACAG 1543
Qy 554 GATGProLeuGluValLeuLeu-----GlyCyProValProLeuGlyVa 569
Db 1544 GCGTGTATAGAGCACTCGACAGAGTGTATACACACGCGCTGCTTCGAGACTTTCAT 1603
Qy 569 LlyGlnLysLeuLeuHisTrpValSerLeuGluYbGlnGlnProAlaIleThrPr 589
Db 1604 CGCCAAAGGCTCTC---TGAGACAGGAATCTTGCAAGTGTGAAAACACACATGA 1660
Qy 589 OGlyAspThrLeuAspAlaPheHisCybLeuPheGluThrGluAspValAr 609
Db 1661 GCAGGAATCTGAAGCCATGAACATC-----AATTCCTTGTAGA 1702
Qy 609 GLeuAlaLeuAsnSerPheGlnGlu-ValTrp-----LeuProIleAsnGlnLeu 627
Db 1703 GTGTGGCACTTATATATCAAGAGATACATCCAAATCAGCCCTGAGCCAGAAATTTGA 1762
Qy 627 sPLeuIleAlaSerSerPheCybLeuGlnHisCybProTyrLeuArgHisIleArgVal 647
Db 1763 AGCTT-----TCTTCAAGTA-----AAAGCTTATAT 1792
Qy 647 sPValYbGlyIlePheProArgAsp-----GluSerAlaGlnAlaCybProValVal 664
Db 1793 CAATCAGGGAACATCCCGATTACTTATGACTTCTTGAAACATTTGCCAATGTGTC 1852
Qy 665 -----ProLeuTrpMetArgAspVal 672
Db 1853 AAGTCTCTGACATTCATTAACGTGACTTTATGAGGAGACTATGCGCTGAGGAAA 1912
Qy 672 hIleuIleGluGluGln-TrpGluAspPheCybSerMetLeuGlyThrHisProHisLeu 691
Db 1913 GCGTCGACAGACACAGGTGC-----AATTCACAT--- 1942
Qy 692 ArgGluLeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCybAla 711
Db 1943 -----GGAAGAGGCCCAAGAACTTACATTC 1969
Qy 712 LysLeuAspArgHisProThrCybLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThr 731
Db 1970 CAG-----CAGGCGCTGTATCTT---GTTCTTCACTGAGAA 2002
Qy 732 ProGluValGlnIleLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsn 751
Db 2003 GCGAATATTCGGA-CTGTGAGGTC-ACATC---CGGAAATTCAGCAAGTTGAAT 2054
Qy 752 LeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCybGlnAlaLeuLysHis 771
Db 2055 -----AAGCAAGATATCATATCTGGGAAAATATTCAGCTCT 2093
Qy 772 ProLysCybLeuLeuGluSerLeuArgLeuAsp-----CybCybGlyLeuThrHis 788
Db 2094 -----GCCAAGAGCTCAGGCTGCAAAATTAAGAGATGTGCTGTGCTGCA 2141
Qy 789 AlaCybTyrLeuLysIleSerGlnIleLeuThrHisSerProSerLeuLysSerLeuSer 808
Db 2142 AGC-----CTAGTTGTGCTCTCAGACCTGTAAAGACATTTATCTCTCATG 2189
Qy 809 LeuAlaGlyAsnLysLeuValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVal 828
Db 2190 GTGGAAGCAGTCCCTCACC-----ATAGAAGATGAGAGGACATC 2231

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Qy 829 SerGlnCybAla---LeuGlnLysLeuIleLeuGluAspCyb----- 841
Db 2232 ACATCTGTAAACAACCTTGAAAACCTTGAGTATCATGATCAAGAAATCAACGCGCTCGG 2291
Qy 842 ---GlyIleThrAlaThrGlyCybGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db 2292 GGTGTCTGACT-----GACAGCTTGCGGTAACTTGAGAAC 2327
Qy 861 LeuThrHisLeuCybLeuSerAsnAsnSerLeuGluYbGlnGlyValAsnLeuLeuCyb 880
Db 2328 CTTAACAAGCTCATTAATGATTAACAATTAAGTAAAGATGATGCTATTAACCTAGCT 2387
Qy 881 ArgSerMetArgLeuProHisCybSerLeuGlnArgLeuMetLeuAsnGlnCybHisLeu 900
Db 2388 GAAGCCCTGAAA-----AAGCTGAAGAAAGATGTATTATTTTCAT----- 2426
Qy 901 AspThrAlaGlyCybGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920
Db 2427 -----TTGACCCAC 2435
Qy 921 LeuSerLeuSerMetAsnProValGluAsp-----AsnGlyValLysLeuLeuCybGlu 938
Db 2436 TTGTCT-----GACATTGAGAGGGAATGAGATTACATAGCTCAAG 2474
Qy 939 ValMetArgGluProSerCybHisLeuGlnAspLeuGluLeuValLysCybHisLeuThr 958
Db 2475 TCTCTGTCAATGAACCTGTGACCTTGAAGAAATTCATTAAGTCTCCTGCGCTGTCT 2534
Qy 959 AlaAlaCybCybGluSerLeuSerCybValIleSerArgSerArgHisLeuLysSerLeu 978
Db 2535 GCAATGACGATGAAGAAATCTAGCTCAGAAATCTTCAATTTGGTCAAACTAGACATTTCT 2594
Qy 979 AspLeuThrAspAlaAlaLeuGlyAspGlyValAlaAlaLeuCybGluGlyLeuLys 998
Db 2595 GATTATTCAGAAATTCATCTGAAAAGATGAAGATGAAGCTTTCATGAACCTGATCAC 2654
Qy 999 GlnLysAsnSerVal----- 1003
Db 2655 AGGATGAACGTGCTAAGAACACTCAGCAGCTGATGCTGCGCGCTGTGAGCGTGA 2714
Qy 1004 -----LeuThrArgLeuGly 1008
Db 2715 GGCAGCTGAGACGCTGTGAAACATTTGAGAGAGTCCCAACCTGTCAGAGCTTGGG 2774
Qy 1009 LeuLysAlaCybGlyLeuThrSerAspCybCybGlyAlaLeuSerLeuAlaLeuSerCyb 1028
Db 2775 TTGAAAACCTGAGACTCAGACATACAGAGATTGAATTTTAGTGCAATTTTGGAAAG 2834
Qy 1029 Asn-----ArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db 2835 AACCTCTGAAAACCTTCCAGCAGTTGAATTTGGCGGAAAATCTGTGAGCAGATGGA 2894
Qy 1047 MetMetLysLeuCybSerAlaPheAlaCybProThrSerAsnLeuGlnIleIleGlyLeu 1066
Db 2895 TGGCTTGCTTCATGCGGTATTT-----GAGAATCTTAACCAATTAAGTGT 2942
Qy 1067 TrpLysTrpGlnTrp-----ProValGlnIleArgLysLeu----- 1078
Db 2943 TTGACTTTAGTAAAGAAATTTCTACCTGATCAGCATTAAGTGAAGAAATTTGCCAA 3002
Qy 1079 -----LeuGluGluValGlnLeuLeuLysProArgValValIle 1091
Db 3003 GTGTTATCCAACTTAATCTTTCTGCAAGAGTAGGCTTGT----- 3044
Qy 1092 AspGlySerTrpHisSerPheAspGluAspArgHisLysIleGlyLeuThrPheArg 1111
Db 3045 -----GGGTGG---CAATTGATGATGATGATCTCAGGTATTAACAGTGCCTTTTAA 3095
Qy 1112 Leu 1112
Db 3096 CTA 3098

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RESULT 10

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US-11-145-631-1
; Sequence 1, Application US/11145631
; Publication No. US2006003409A1
; GENERAL INFORMATION:
; APPLICANT: Bectin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-32901
; CURRENT APPLICATION NUMBER: US/11/145,631
; PRIOR FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3133
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(3107)
; US-11-145-631-1

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Alignment Scores:
Pred. No.: 1.51e-14 Length: 3133
Score: 276.00 Matches: 232
Percent Similarity: 37.30% Conservative: 157
Best Local Similarity: 22.24% Mismatches: 349
Query Match: 3.90% Indels: 308
Gaps: 51

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US-10-066-521-6 (1-1344) x US-11-145-631-1 (1-3133)

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Qy 191 ValLeuHisGlySerGlyLeGlyLysSerAlaLeuAlaArgAlaValLeuCys 210
    ::::: ||||| ::::: |||||
Db 531 ATCTTGAAGGGAATCTGGCAAGGCAAGTCACTGCTGCGAGCCGATGCGATGCTC 590
Qy 211 TTPAlaGlnGlyGlyLeuTrGln--GlyMetSerSerValPhePheLeuProVal 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 591 TGGGGCTCCGGAAGTCAAGGCTCTGACCAAGTTCAATTCGCTTCCTCCGCTC 650
Qy 230 ArgGluMetGlnArgGlyLysGluSerSerValThrGluPheLeuSerArgGluTrpPro 249
    ::::: ||||| ::::: |||||
Db 651 AGCAGGGCCCAAG-----GTTGACTTTTGAACCTCTGTGATCAACTCTCG 698
Qy 250 Asp-----SerGlnAlaProValThrGluLeuMetSerArgProGlu 263
    ||||| ||||| ||||| |||||
Db 699 GATTTACCTGGCAATCAAGAGCAAGCACTTACGCGCATGCTGCGAGCTGCGGAG 758
Qy 264 ArgLeuLeuPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 759 AGGGTCTCTTCTTCTTGTGATGCTACATGAATTC-----AAGCCC 800
Qy 284 LysLeuCysLysAspTrpAlaGluLysGlnProPheThrLeuLeuLeuLeuLeuLeu 303
    ::::: ||||| ::::: |||||
Db 801 CAGAACTGCCCAAGAA-----ATCGAAGCCCTGATA 830
Qy 304 ArgLysValLeuLeuProGluSerPheLeuLeuValThr----- 316
    ::::: ||||| ::::: |||||
Db 831 AAGGAAGAACCAACCGCTTCAAGACATGCTATCGTCACTACACATCACTGAGTGC 890
Qy 317 ---ValArgAspValGlyThrGluLysLeuLysSerGlnValValSerProArgTrpLeu 335
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 891 CACATACGGCGAGTTTGCGCC-----CTGACTCTGAGGTGGGAGTATGACAGAA 944
Qy 336 LeuValArgGlyLysSerGlyGluGlnArgGlyLeuLeuLeuLeuLeuLeuLeuLeu 944
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 945 AGCCGCCAGGCTCTTCATCCAGAAAGTGTGATCAAGAGCTTGTGAAGGCTTGTC 1004
Qy 356 GluHisGlnLysThrGlnGlyLeuArgAlaLeuMetAsnAsnArgGluLeuLeuAspGln 375

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Db 1005 CAATTCAGAAATCCAGGTGCTGAGGAATCTCATG----- 1040
Qy 376 CysGlnValProAlaValGlySerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuVal 395
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1041 ---AAGCCCTCTCTTGTGTGATCACTTG---GCAATTCAGAG----- 1082
Qy 396 GlyLysSerValAlaProPheAsnGlnThrGlyLeuHisAlaAlaPheValPhe 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1083 GGTGAAGATGATTCACCTCTCACACAAACAGCGTTTCAT-----ACCTTC 1133
Qy 416 HisGlnLeuThrProArgGlyValValArgArgCysLeuAsnLeuGlnGluArgVal 435
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1134 TATGATCTG-----TTGATACAGAAAAACAAACAAATGAAGTGTGGCT 1181
Qy 436 LeuLysArgPheCysArg-----MetAlaValGlnGlyValTrp 448
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1182 GCAAGTACTTCAATTCGAGACCTGAGACCACTGAGACCTAGCTCGAGGGTGTTC 1241
Qy 449 AsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyLysArg 468
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1242 TCCCAAGATTTGATTTCCAGATGCAAGAT-----GTGTCAGCGTGAATGAG----- 1289
Qy 469 LeuArgAlaLeuPheHisMetAsnLeuLeuLeuProAspSerHisCysGlnGlyTrp 487
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1290 -----GATGTCCTGCTGACCACTGGGCTCTCTGTAATATATACA 1328
Qy 488 -----TyrThrPhePheHisLeuSerLeuGlnAspPheCysAla 500
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1329 GCTCAAGTTCAGCAAGCAAGTAAATTTTTCACATTCATCCAGAGTACACAGCA 1388
Qy 501 Ala-----LeuTyrTrpValLeuGlnGlyLeuGlnLeuProAlaLeuCysProLeu 518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1389 GAGCAAGACTCAGCAGGTTATTGAGCTCATGAGCCAG----- 1430
Qy 519 TyrValGlnLysThrLysArgSerMetGluLeuLysGlnAlaGlyPheHis----- 535
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1431 -----GAGGTGACCAAGGGGAATGTACTTCCAGAAAT--GGTTTCCATTTCCGACAT 1483
Qy 536 ---IleHis--SerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGlnAspValAr 554
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1484 TACATCACTTATAGCAGCTCTCCGATCACCTGTGGGTCTATCTGGAAGCCACAG 1543
Qy 554 GArgProLeuGlnValLeuLeu-----GlyCysProValProLeuGlyVal 569
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1544 GCGTGTATGAAGACCTCCAGACAGTATCAACAGCGCTGCTCGAATTTTCAT 1603
Qy 569 LysGlnLysLeuLeuHisTrpValSerLeuLeuGlnGlnProAsnAlaThrTrp 589
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1604 CGCCAGAGGCTCTC---TGGAGACAGAAATCTTGCMAAGTGTGAAAAACACACTGA 1660
Qy 589 OGlyAspThrLeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValAr 609
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1661 GCAGAAATTTGAAAGCCATAACATC-----AATTCCTTTGTAGA 1702
Qy 609 GLeuAlaLeuAsnSerPheGlnGlu--ValTrp-----LeuProIleAsnGlnAsnLeu 627
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1703 GTGTCGATCATTTATATCAAGAGTATCATCAATTCAGCCCTGAGCCAAAGATTGA 1762
Qy 627 sPheLeuLeuAspSerPheCysLeuGlnHisCysProTyrLeuArgLysLeuArgVal 647
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1763 AGCTT-----TCTTTCAAGGTA-----AAGCTTATATAT 1792
Qy 647 sPValLysGlyLysPheProArgAsp-----GluSerAlaGluAlaCysProValVal 664
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1793 CAACTCAGGAAACATCCCAATTACTTATTTGACTTTTGAACATTTGCCCAATTTGCC 1852
Qy 665 -----ProLeuTrpMetArgAspLysTrp 672
    ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1853 AAGTGTCTGGACTTATTAATGACTTTTATGGGAGGTATGCTTCACTGAGGAAAA 1912
Qy 672 hTrpLeuLeuGlnGln--TrpGluAspPheCysSerMetLeuGlyThrHisProHisLeu 691
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db      1913 GCCTGACGAGACACAGCTGG-----ATTCACAT--- 1942
Qy      692 ArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgIleMetLysThrLeuCyseAla 711
Db      1943 -----GGAGAGAGCCGCCAGAACCTCAGATTCC 1969
Qy      712 LysLeuArgHisProThrCysLeuValIleGlnThrLeuMetPheArgAsnAlaGlnIleThr 731
Db      1970 CAG-----CAGGGCTGTACTTT-----GTTCTTCAACTGGAA 2002
Qy      732 ProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsn 751
Db      2003 GCAGGAATTCAGCA-CTCTGAGGTC-ACACTC-----CGGATTTGAGCAAGTTGAT 2054
Qy      752 LeuGlyGlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLysHis 771
Db      2055 -----AAGCAAGATATCATATCTGGGAAAAATTCAGCTCT 2093
Qy      772 ProLysCysLeuLeuGluSerLeuArgLeuAsp-----CysCysGlyLeuThrHis 788
Db      2094 -----GCCACAGCCTCAGCTGCAATAAAGACATGCTGTGTGCTGCA 2141
Qy      789 AlaCysThrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSer 808
Db      2142 AGC-----CTCAGTTGTGCTCTCAGCACCTGTAAAGACATTATTCTCTCATG 2189
Qy      809 LeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgVal 828
Db      2190 GTGAGAGCCAGTCCCTCACC-----ATAGAAGATGAGAGGACATC 2231
Qy      829 SerGlnCysAla---LeuGlnLysLeuIleLeuGluAspCys----- 841
Db      2232 ACATCTGTAAACAACTGAAACCTTGAGTATCTATGACTTACAGATCAACGCGTCCG 2291
Qy      842 ---GlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db      2292 GGTGCTCTGACT-----GACAGCTGGGTAAGTCTGAGAAC 2327
Qy      861 LeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyAsnGlyValAsnLeuLeuCys 880
Db      2328 CTTACAAAGCTCATTAATGATTAACATAAGATGAAGATGAAGATGATAAATAACTACT 2387
Qy      881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900
Db      2388 GAAGGCTGAAA-----AACCTGAAGAGATGTTTATTTTCAT----- 2426
Qy      901 AspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHis 920
Db      2427 -----TTGACCCAC 2435
Qy      921 LeuSerLeuSerMetAsnProValGluAsp-----AsnGlyValLysLeuLeuCysGlu 938
Db      2436 TTGTCT-----GACATTGAGAGAGGAGATGATTAATCACTACTCAAG 2474
Qy      939 ValMetArgGluProSerCysHisIleGlnHisLeuGluLeuValLysCysHisIleLeu 958
Db      2475 TCTGTGTAAGTAAACCTGTGATCCTTGAAGAAATTCATTAATGTTCTCTGCTGTGCT 2534
Qy      959 AlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978
Db      2535 GCAATTCAGTGAATAATCTAGCTCAGATCTTCAACATTTGTCGAATTCAGATTCCTT 2594
Qy      979 AspLeuThrAspAsnAlaLeuGlyValAspGlyValAlaAlaLeuCysGluGlyLeuLys 998
Db      2595 GATTATATCAGAAAATTACTCTGGAAGAAAGATGAAGATGAACTCTTCATGAACTGATCAG 2654
Qy      999 GlnLysAsnSerVal----- 1003
Db      2655 AGGATGAACGTGTGAACAGCTCAACGCACTGATGCTGCTGCGGCTGTGACCTGCA 2714
Qy      1004 -----LeuThrArgLeuGly 1008
Db      2715 GGCACCTGAGAGCGCTGTGAACAATTGAGAGAGTCCACAACTGCTCAAGCTTGGG 2774

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Qy      1009 LeuLysAlaCysGlyLeuThrSerAspCysGluAlaLeuSerLeuAlaLeuSerCys 1028
Db      2775 TTGAAAACCTGAGACCTCAGATTAACAGATTTGAATTTTAGTGCATTTTGGAAAG 2834
Qy      1029 Asn-----ArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db      2835 AACCTCTGAAAACCTTCAGACAGTGAATTTGGCGGAAATCTGTGAGCAGATGAGA 2894
Qy      1047 MetMetLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu 1066
Db      2895 TGGCTTGCTTCATGCGGTGATTT-----GAGATCTTAAGCAATTTAGTGT 2942
Qy      1067 TrpLysTrpGlnLys-----ProValGlnIleArgLysLeu----- 1078
Db      2943 TTTAATTACTTACTTAAGATTTTCTACTTCATTCAGATTAAGTCAAGAAACCTTAGCAA 3002
Qy      1079 -----LeuGluGluValGlnLeuLeuLysProArgValValIle 1091
Db      3003 GTGTATTCAGATTAACTTTCTGCAAGAACCTTAGCTTGT----- 3044
Qy      1092 AspGlySerTrpHisSerPheAspGluAspArgHisLysIleGlyLeuThrPheArg 1111
Db      3045 -----GGGTGG---CAATTGATGATGATGATCTCAGTGTATTATACAGTGTCTTAA 3095
Qy      1112 Leu 1112
Db      3096 CTA 3098

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## RESULT 11

US-11-145-631-6  
Sequence 6, Application US/11145631  
Publication No. US2006003409A1

## GENERAL INFORMATION:

APPLICANT: Bertin, John  
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THEREOF  
FILE REFERENCE: 07334-329001  
CURRENT APPLICATION NUMBER: US/11/145,631  
CURRENT FILING DATE: 2005-06-06  
PRIOR APPLICATION NUMBER: US/09/841,739  
PRIOR FILING DATE: 2001-08-29  
PRIOR APPLICATION NUMBER: US 09/697,089  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/161,822  
PRIOR FILING DATE: 1999-10-27  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 3612  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-145-631-6

## Alignment Scores:

Pred. No.:	1.9e-14	Length:	3612
Score:	276.00	Matches:	254
Percent Similarity:	37.03%	Conservative:	193
Best Local Similarity:	21.04%	Mismatches:	423
Query Match:	3.90%	Indels:	340
DB:	8	Gaps:	56

US-10-066-521-6 (1-1344) x US-11-145-631-6 (1-3612)

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Qy      17 CysLeuTrpGluLeuAspLysGluLubegInThrPheLysGluLeuLeuLysLys 36
Db      541 TGCTGCGAAGAGGTGAGCAGAGATGCTGCTGAGGATCATTCACATGATTTTGAAG 600
Qy      37 SerSerGluSerTrpThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGlu 56
Db      601 GGTTCAGAGTCC-----TGTAACTC----- 621
Qy      57 CysLeuAlaLeuLeuHisGlyLysTrpGlyAlaSerLeuAlaTrpAlaThrSerIle 76

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Db 622 -----TTTCTTAATCCCTTAAGAGAGTGG-----AACTAT 651  
 Qy Ser1IlePheGluAsnMetAspLeuAaIgtThrLeuSerGluValAaIArgAspArmMetLys 96  
 Db 652 CCTCTATTTAGAGACTTGAATGACAAAGTTTGGAGAGACACAAATTTGGGCTTCTTT 711  
 Qy Lys1IleSerGlnA1aMetGluGluGluGluValA1aThrA1aA1aGluThrGluGluGluGlu 116  
 Db 712 AACATCACCTCTTCTCTAATAGCTTTTTCATCAGACATCAGAAAGAGACTTGGAGAT 771  
 Qy 117 IleSerGlnA1aMetGluGluGluGluValA1aThrA1aA1aGluThrGluGluGluGlu 136  
 Db 772 TTGGCTCAGATTTAAAGACTTGTACCAATCCCACTTTTCTTGAACCTTTATCCCTT 831  
 Qy 137 G1yG1yAspThrTrpAspTrpLysSerHisValMetThrLysPheA1aGluGluGluAsp 156  
 Db 832 GGTGAAGATATTT---GACATTTATTTTAACTTGAAGAACCTTCACAGAACTGTCTG 888  
 Qy 157 ValArgAspSerPheGluAsnThrA1aA1aAspTrpProGluMetGlnThrLeuA1aG1y 176  
 Db 889 TGGAGGAAAGACCAACACATCACCGGTGGAGAGAGCTGACCTGAAATGGCTCTGACAG 948  
 Qy 177 AlaPheAspSerAspAspG1yTrpG1yPheArgProArgThrValValMetHisG1yLysSer 196  
 Db 949 GCTCTTCAGAGC-----CCTGCATCATTTGAAGGGGAATCT 984  
 Qy 197 G1y1IleG1yLysSerA1aLeuA1aArgArg1IleValLeuGluSerTrpA1aGluG1yLys 216  
 Db 985 GGCAAAAGGCAAGTCTCACTGTGCTGACAGGAATTCCTGCTGAGGCTCCGAAATGTC 1044  
 Qy 217 TyrGln---GlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLys 235  
 Db 1045 AAGGCTGTACCAAGTTCAATGCTGTCTTCTCTCCGTCCAGACAGAGGCCAG----- 1098  
 Qy 236 LysGluSerSerValThrGluPhe1IleSerArgGluTrpProAsp----- 250  
 Db 1099 ---GGTGAACCTTTTGAACCCCTGTGATCACTCTGTGATATATATACCTGGACAAATC 1152  
 Qy 251 ---SerGlnA1aProValThrGlu1IleMetSerArgProGluArgLeuPhe1Ile 269  
 Db 1153 AGGAAAGACATTCATGCGCATCTGCTGAACTGGGCGACAGAGGCTTCTTCTTCTT 1212  
 Qy 270 AspG1yPheAspAspLeuG1ySerValLeuAsnAsnAspThrLysLeuG1yLysAspTrp 289  
 Db 1213 GATGGCTACAAATGAATTC-----AAGCCCCAGAACTGCCCGCAGAA--- 1251  
 Qy 290 AlaGluLysGlnProPheThrPhe1IleArgSerLeuLeuArgLysValLeuLeuPro 309  
 Db 1252 -----ATCGAAGCCCTGATTAAGGAAACCAACCGCTTC 1284  
 Qy 310 GluSerPheLeu1IleValThr-----ValArgAspValG1y 321  
 Db 1285 AAGAACATGGCTCATCTGCACCACTACACATGAGTCCCTGAGGCAATACGGAGTTTGGT 1344  
 Qy 322 ThrGluLysLeuLysSerGluValValSerProArgTyrLeuLeuValArgG1y1IleSer 341  
 Db 1345 GCC-----CTGACTGCTGAGGTGGGGATATGACAGAAAGACAGCCGACGCTCATC 1398  
 Qy 342 G1yG1yGluGlnArg1IleHisLeuLeuLeuGluArgG1y1IleG1yGluHisGlnLysThrGln 361  
 Db 1399 CGAAGATGCTGTCAAGAGACTTGTGAAAGCTTGTGCTCAAAATTCAGAAATCCAGG 1458  
 Qy 362 G1yLeuArgA1a1IleMetAsnAsnArgGluLeuLeuAspGlnG1ySerGlnValProA1aVal 381  
 Db 1459 TGCTTGAGGAATCTCATG-----AAGACCCCTCTCTTT 1491  
 Qy 382 GlySerLeuLeuCyValA1aA1aLeuGlnLeuGlnAspValValG1yGluSerValA1aPro 401  
 Db 1492 GTGGTCACTACTTGT---GCAATCCAGATG-----GGTGAAGAGTCAATTCACAC 1536  
 Qy 402 PheAsnGlnThrLeuThrG1yLeuHisA1aA1aPheValPheHisGlnLeuThrProArg 421  
 Db 1537 TCTCACACACAAACAGCTGTTCAT-----ACCTTATATGATCTG----- 1578

Qy 422 G1yValValArgArgCyLeuAsnLeuGluGluArgValValLeuLysArgPheCyArg 441  
 Db 1579 -----TTGATACAGAAAACAAACACAAACATAAAGGTGTGGCTGCAGTGCATTCACGG 1635  
 Qy 442 -----MetA1aValGluG1yValTrpAsnArgLysSerValPhe 454  
 Db 1636 AGCCTGGACCACTGTGGAGACTTACGCTTGGAGGGGTGTGTTCTCCCAAGTTTGATTTG 1695  
 Qy 455 AspG1yAspAspLeuMetValGlnG1yLeuG1yGluSerGluLeuArgA1aLeuPheHis 474  
 Db 1696 GAATCGAGAT-----GTGTCAGCGTAAATGAG----- 1725  
 Qy 475 MetAsn1IleLeuLeuProAspSerHisCyGluGluLys----- 487  
 Db 1726 ---GATGCTGCTGACCACTGGGCTCTCTGTGAATATATACAGTCAAGGTTCAAGCCA 1782  
 Qy 488 ---TyrThrPhePheHisLeuSerLeuGlnAspPheCyA1aA1a-----LeuTyrTyr 504  
 Db 1783 AAGTATTAATTTCTTTCACAGATTCACAGAGTACACAGACAGACAGACTTCAGAGCT 1842  
 Qy 505 ValLeuGluG1yLeuGlu1IleGluProA1aLeuCySerProLeuTyrValG1yLysThrLys 524  
 Db 1843 TTAATGACGTCTCATGAGCCAGAG-----GAGGTGACCAAG 1878  
 Qy 525 ArgSerMetGluLeuLysGlnA1aG1yPheHis-----1IleHis-SerLeuTyr 540  
 Db 1879 GGGAAAGTATTACTTGCAGAAAT---GGTTTCATTTGCGACATTAATCATTCATTATAGCAG 1937  
 Qy 540 PheLysArgPheLeuPheG1yLeuValSerGluAspValArgArgProLeuGluValLe 560  
 Db 1938 CCGTCCCGGTGACACCTGTGGTGCATCTGTGAAAGCCACAGAGGCTGTATTGAAGACCT 1997  
 Qy 560 LysLeu-----GlyCySProValProLeuG1yValLysGlnLysLeuLeuHis 575  
 Db 1998 GCGACAGTATATCAACACAGGCTGCTCTTCCGACTTTCATGCGCAAGAGGCTCTC-- 2055  
 Qy 575 sTrpValSerLeuLeuG1yGlnGlnProAsnA1aThrThrProG1yAspThrLeuAspA1 595  
 Db 2056 -TGGAGACAGAAATCTTGGCAAGGTGAAACACACACTGACAGCAAGAAATTCGAAAGC 2114  
 Qy 595 arPheHisCyLeuPheGluThrGlnAspLysGluPheValArgLeuA1aLeuAsnSerPh 615  
 Db 2115 CATTAACATC-----AATTCCTTGTAGAGTGTGGATTCATTTATA 2156  
 Qy 615 eGlnGlu-ValTrp-----LeuPro1IleAsnGlnAsnLeuAspLeu1IleAspSerP 633  
 Db 2157 TCAAGAGATACATCCAAATCAGCCCTGAGCCCAAGATTTGAAGCTT---TCTT 2207  
 Qy 633 heCySLeuGlnHisCySProTyrLeuArgLys1IleArgValAspValLysG1y1IlePheP 653  
 Db 2208 TCAAGTAA-----AAAGCTTATATATACACTACAGGAAACATCCC 2246  
 Qy 653 roArgAsp-----GluSerA1aGluA1aCySProValVal----- 664  
 Db 2247 CGATTACTTATGACTTCTTGAACATTTGGCCCAATTTGGCAAGTCCCTGACCTTCAT 2306  
 Qy 665 -----ProLeuTrpMetArgAspLysTrpThrLeu1IleGluGluGln- 677  
 Db 2307 TAAACTGACTTTTATGGGAGAGTATGCTTCATGAGGAAGAGCTGCAGAAAGCACAGG 2366  
 Qy 678 TrpGluAspPheCySerMetLeuG1yThrHisProHisLeuArgGlnLeuAspLeuG1y 697  
 Db 2367 TGG-----AATCCACAT----- 2378  
 Qy 698 SerSer1IleLeuThrGluA1aMetLysThrLeuCyValA1aLysLeuAspThr 717  
 Db 2379 -----GGAAAGAGGCCCAAGAACTTACATTCACAG----- 2408  
 Qy 718 CyLeuSer1IleGlnThrLeuMetPheArgAsnA1aGln1IleThrProG1yValGlnHisLeu 737  
 Db 2409 -----CAGGGCTGTATCTTT---GTTCTTCAACTGGAAGCAGGAATTCAGGA-CTC 2455

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QY 738 TTPATGILELWELALASARGASLEULARGSERLEULASLEULGLYLTHTHISLEU 757
DB 2456 TGGAGGTC-ACACTC-----CGGATTTTCAGCAAGTTGAT----- 2490
QY 758 LysGluValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGlu 777
DB 2491 ---AGCAAGATATCAGATATCTGGGAAATATTCAGCTCT-----GCCACA 2535
QY 778 SerLeuArgLeuAsp-----CysCysGlyLeuThrHisAlaCysTyrLeuLysIle 794
DB 2536 AGCTTCAGGCTGCACAAATTAAGAGATGCTGCTGTGGCTGGAAGC-----CTC 2583
QY 795 SerGlnIleLeuThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysVal 814
DB 2584 AGTTGGCTCTCAGACCTGTGAAGAACATTTATTTCTTCATGCTGGAAGCCAGTCCCTC 2643
QY 815 ThrArgGlnGlyValMetProLysSerArgAlaLeuArgValSerGlnCysAla--Leu 833
DB 2644 ACC-----ATAGAGATGAGAGACACATCATCTGTAAACAAACCTG 2685
QY 834 GlnLysLeuIleLeuGluAspCys-----GlyIleThrAlaThr 846
DB 2686 AAAACCTTGAGTATTCATGACCTTACAGATCAACGGCTCGGCTGTGCTGACT----- 2739
QY 847 GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
DB 2740 -----GACAGCTTGGGTAACTTGAAGAACCTTTCACAAAGCTCTAATG 2781
QY 867 SerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetCysLeuPro 886
DB 2782 GATAACATTAAGATGAATGAAGAGATGCTTAATAACTAGTGAAGGCTGAAA----- 2835
QY 887 HisCysSerLeuGlnArgLeuMetLeuLysGlnCysHisLeuAspThrAlaGlyCysGly 906
DB 2836 ---AACCTGAAGAGATGCTGTATTATTCAT----- 2862
QY 907 PheLeuAlaLeuAlaLeuMetClyAsnSerTrpLeuHisLeuSerLeuSerMetAsn 926
DB 2863 -----TTGACCCCACTTGTCT----- 2877
QY 927 ProValGluAsp-----AsnGlyValLysLeuLeuCysGluValMetArgGluProSer 944
DB 2878 -----GACATTGAGAGAGGAGATGATTACATATGCAAGTCTCTGCAAGTGAACCC 2928
QY 945 CysHisLeuGlnAspLeuGlnLeuValLysCysHisLeuThrAlaAlaCysCysGluSer 964
DB 2929 TGTGACCTTGAAGAAATTCATTAATGCTCTGCTGCTGTGCAAAATGCACTGAATAATC 2988
QY 965 LeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAla 984
DB 2989 CTAGCTCAGAAATCTTTCACAAATTTGCTCAACTGAGCATTTCTTGATTTATCAGAAAATTAC 3048
QY 985 LeuGlyAspGlyGlyValAlaAlaLeuCysGlnGlyLeuLysGlnLysAsnSerVal--- 1003
DB 3049 CTGGAAGAAAGATGAATGAATGAACTCTTTCATGAATGATGACAGATGAACCTGTAAGA 3108
QY 1003 ----- 1003
DB 3109 CAGCTCACCGCAGCTAGTCTGCCCTGGGCTGTGACGTGCAGAGCAGCCTGACGCTG 3168
QY 1004 -----LeuThrArgLeuGlyLeuLysAlaCysGlyLeu 1014
DB 3169 TTGAAACATTTGGAGAGAGGTCCCAACATCTGTCAGCTTGGGTTGAAAACCTGAGACATC 3228
QY 1015 ThrSerAspCysCysGluValaLeuSerLeuAlaLeuSerCysAsn-----ArgHisLeu 1032
DB 3229 ACAGATACAGAGATTAAGATTTTAGGTGATTTTGGAAAGAACCCCTGTAATAAATTC 3288
QY 1033 ThrSerLeuAsnLeuValGlnAsnAsnSerProLysGlyMetMetLysLeuCysSer 1052
DB 3289 CAGCAGTGAATTTGGCCGGGAAATGCTGTGAGCAGATGATGGCTTCATGAGGT 3348
QY 1053 AlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyr--- 1071

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DB 3349 GATATT-----GAGAAATCTTAAGCAATGATGTTTGTGACTTAACTTAATAA 3396
QY 1072 -----ProValGlnIleArgLysLeu----- 1078
DB 3397 GAATTTCTACTGATATCCAGCATTTAGTCAAGAAACTTACCCCAAGTTTATCCAACTTAAT 3456
QY 1079 ---LeuGlnGluValGlnLeuLeuLysProArgValIleLeuAspGlySerTrpHisSer 1097
DB 3457 TTCTGCAAGAGAGCTAGGCTTGT-----GGGTGG---CAA 3489
QY 1098 PheAspGluAspAsp 1102
DB 3490 TTTGATGATGATGAT 3504

RESULT 12
US-11-145-631-4
; Sequence 4, Application US/11145631
; Publication No. US2006003409A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/11/145, 631
; PRIOR FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/841, 739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697, 089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161, 822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3612)
; US-11-145-631-4

Alignment Scores:
Pred. No.: 1,91e-14 Length: 3615
Score: 276.00 Matches: 254
Percent Similarity: 37.03% Conservative: 193
Best Local Similarity: 21.04% Mismatches: 423
Query Match: 3.90% Indels: 340
DB: 8 Gaps: 56

US-10-066-521-6 (1-1344) x US-11-145-631-4 (1-3615)
QY 17 CysLeuTyrGlnLeuAspLysGlnGluPheGlnThrPheLysGlnLeuLysValLys 36
DB 541 TGTCTCAGAGAGGTGAGACAGATGCTCTGAGGAGATCATTCATGATTTTGAAGAAAG 600
QY 37 SerSerGlnSerThrThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGlu 56
DB 601 GGTTAAGAGTCC-----TGTAACTCT----- 621
QY 57 CysLeuAlaLeuLeuLeuHisGlnLysTyrGlyAlaSerLeuAlaTrpAlaThrSerIle 76
DB 622 -----TTCTTAATCCCTTAAGAGACTGG-----AACTAT 651
QY 77 SerIlePheGluAsnMetAsnLeuArgThrLeuSerGlnLysValaArgAspMetLys 96
DB 652 CCTTAATTCAGCACTTGAATGACAAAGATTGAGAGACACAGAAATGGGCTTCTTT 711
QY 97 LysIleSerGlnAlaMetGlnGlnGlnGlnLysAlaThrAlaAlaGluThrGlnGlnGln 116
DB 712 AACATACCTCTTCTTAATGAGTTTTCATTCAGATCATCGAAGAGACTTGAACAT 771
QY 1117 IleSerGlnAlaMetGlnGlnGlnGlnLysAlaThrAlaAlaGluThrGlnGlnGlnHis 136

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Db      772 TTGGCTCAGGATTTAAAGACTTGTACCATACCCCACTTTTCGAAGCTTTATCCCTT 831
Qy      137 GYGLVAspThrTrpAspTrpTyrLysSerHisValMetThrLysPheAlaGluGluAsp 156
Db      832 GGTGAAGATATTT---GACATATATTTTAACTGTAAAGACACTTACAGAACTGTCTCTG 888
Qy      157 ValArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGly 176
Db      889 TGGAGAGAGACCAACCATCAACCGGTGAGAGAGTGAACCGTGAATGACCTCTGACAG 948
Qy      177 AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyLysSer 196
Db      949 GCTCTTCAGAGC-----CCCTGCATCATTTGAAGGGGAACTCT 984
Qy      197 GYVLeuLysSerAlaLeuAlaArgArgGLeuValLeuGluSerProAlaGlnGlyLeu 216
Db      985 GGCAGAAAGCAAGTCTGCTGTCGACGCGAATGCTGCTGGGCTCCGAAAGTGC 1044
Qy      217 TyrGln---GlyMetPheSerTyrValPhePheLeuProValArgGluMetGlnArgLys 235
Db      1045 AAGGCTTGACCAAGTTCAATTCGTCTCTCTCTCCGTCCGTCAAGAGGCCAG----- 1098
Qy      236 LysGluSerSerValThrGluPheLeuSerArgGluTrpProAsp----- 250
Db      1099 ---GGTGCACCTTTTGAACCCCTCTGTGATCAACTCTCGATATACCTGACACATC 1152
Qy      251 ---SerGlnAlaProValThrGluLeuMetSerArgProGluArgLeuLeuPheLeu 269
Db      1153 AGGAAGACAGCATTCATGGCCAGTCTGTAAAGCTGGCGAGAGGGTCTTTCTCTTCTT 1212
Qy      270 AspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCybLysAspTrp 289
Db      1213 GATGGCTACATGATTC-----AAGCCCAAGAACTGCCAGAA--- 1251
Qy      290 AlaGluLysGlnProProPheThrLeuLeuArgSerLeuLeuArgLysValLeuLeuPro 309
Db      1252 -----ATCGAAGCCCTGATAAAGAAACCAACCGCTTC 1284
Qy      310 GluSerPheLeuLeuValThr-----ValArgAspValGly 321
Db      1285 AAGAACAATGGTCATGTCACCACTACCACTGAGTGCCTGAGGACCATTAACGCACTTTGGT 1344
Qy      322 ThrGluLysLeuLysSerGluValValSerProArgTrpLeuLeuValArgGlyLysSer 341
Db      1345 GCC-----GTGACTGCTGAGGTGGGGATATGACAGAAGACAGGCCGACGCTCATC 1398
Qy      342 GlyGluGlnArgGlyLeuHisLeuLeuGluLysArgGlyLeuGlyLeuHisGlnLysThrGln 361
Db      1399 CGAAGAACTGCTGATCAAGAGAGCTTGCTGAAGGCTTGCTCCAAATTCAGAAATCCAGG 1458
Qy      362 GlyLeuArgAlaLeuMetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaVal 381
Db      1459 TGCCTGAGAAATCTCATG-----AAGACCCCTCTCTCTT 1491
Qy      382 GlySerLeuLeuCybValAlaLeuGlnLeuGlnAspValValGlyGluSerValAlaPro 401
Db      1492 GTGGTCACTACTCTT---GCAATCCAGATG-----GGTGAAGAGTTCAC 1536
Qy      402 PheAsnGlnThrLeuThrArgLysLeuHisAlaAlaPheValPheHisGlnLeuThrProArg 421
Db      1537 TCTCACACACAAACACGCTGTTCCAT-----ACCTTCTATGATCTG----- 1578
Qy      422 GYValValAlaArgGlySerLeuAsnLeuGluGluArgValValLeuLysArgPheCysArg 441
Db      1579 ---TTGATACAGAAACAAACACAAACATTAAGGTGTGCTGCAAGTCACTTATTCGG 1635
Qy      442 -----MetAlaValGluGlyValTyrAsnArgLysSerValPhe 454
Db      1636 AGCCTGAGACCACTGTGAGACCTAGCTCTGAGGGGTGTCTCCCAAGTTGATTC 1695
Qy      455 AspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGluLeuArgAlaLeuPheHis 474

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Db      1696 GAACTGACAGAT-----GTCTCAGCTGATAG----- 1725
Qy      475 MetAsnLeuLeuProAspSerHisCysGluGluTyr----- 487
Db      1726 ---GATCTCTGCTGACAACTGGGCTCTCTGTGAATATACAGTCAAGATTCAAGCCA 1782
Qy      488 ---TyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAla-----LeuTyrTyr 504
Db      1783 AAGTATTAATTTCTTCAACAAGTCACTTCAGAGATGACAGCAGACGAAAGTCAAGCACT 1842
Qy      505 ValLeuGluGlyLeuGluGlnProAlaLeuCybProLeuLysValGlyLysThrLys 524
Db      1843 TTAATGACGTTCATAGACCAAG-----GAGGTGACCAAG 1878
Qy      525 ArgSerMetGluLeuLysGlnAlaGlyPheHis-----IleHis-SerLeuTyr 540
Db      1879 GGGAAATGCTTACTTGCAGAAAT---GGTTTCCATTTTGGACATTAACATTCCTATAGCAG 1937
Qy      540 pMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLe 560
Db      1938 CTGCTCCGGTACACCTGTGGGTCACTGTGGAAGCCACAGGGGCTGTATGAAGCACT 1997
Qy      560 uLeu-----GlyCybProValProLeuGlyValLysGlnLysLeuLeuHis 575
Db      1998 CGACAGCATGTATCAACAGGCTGCTCTTCGACATTCATGCGCCAGAGGCTCTC-- 2055
Qy      575 sTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAl 595
Db      2056 -TGGAGACAGAAATCTTTGCAAGGTGGAACACACACAGTCAAGACAAATTCGAAAGC 2114
Qy      595 asPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPh 615
Db      2115 CATTAACATC-----AATTCCTTGTGAGTGTGGCTCATCATTTATA 2156
Qy      615 eGlnGln-ValTrp-----LeuProIleAsnGlnLeuAspLeuLeuAlaSerSerP 633
Db      2157 TCAAGAGATGATACCAATCAAGCTCTGAGCCAGCAAGATTTGAAGCTT-----TCTT 2207
Qy      633 heCysLeuGlnHisCysProTyrLeuArgLysIleArgValAspValLysGlyLLePheP 653
Db      2208 TCAAGGTA-----AAGCTTATATATATCAACTCAGAGAAATCC 2246
Qy      653 roArgAsp-----GluSerAlaGluAlaCybProValVal----- 664
Db      2247 CGATTACTATTTGACTCTTTGAACATTTGGCCCAATTTGCAAGTGCCTGCACTTCAT 2306
Qy      665 -----ProLeuTrpMetArgAspLysThrLeuIleGluGln- 677
Db      2307 TAAACTGACTTTTATGGGAGACTATGGCTTCATGGGAAAGGCTGCAGAAAGACACAGG 2366
Qy      678 TrpGluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGly 697
Db      2367 TGG-----AATCCACAT----- 2378
Qy      698 SerSerIleLeuThrGluAlaMetLysThrLeuCybAlaLysLeuAspArgHisProThr 717
Db      2379 -----GGAAAGAGGCCCAAGAACTTACATTCGCCAG----- 2408
Qy      718 CysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeu 737
Db      2409 ---CAGGGCTGTATCTTT---GTTCTTCACTGGAAGACAGAAATTCAGAG-CTC 2455
Qy      738 TrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeu 757
Db      2456 TGGAGGTC-AACATC-----CGGAAATTCAGAAATTCGAAAT----- 2490
Qy      758 LysGluGluAspValArgMetAlaCysGlnAlaLeuLysHisProLysCysLeuLeuGlu 777
Db      2491 ---AAGCAAGATATCAAGATATCTGGGGAATAATTCAGCTCT-----GCCACA 2535
Qy      778 SerLeuArgLeuAsp-----CysCysGlyLeuThrHisValaCysTyrLeuLysIle 794
Db      2536 AGCCTCAGGCTGCAATTAAGAGATGTGCTGTGTGCTGGAAGC-----CTC 2583

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QY 795 SerGlnIleuThrThrSerProSerLeuSerLeuAlaGlyAsnIysVal 814
DB 2584 AGTTGGGCTCTGAGCCTTGAAGAACATTATTTCTTCATGAGTGAAGCCAGTCCCTC 2643
QY 815 ThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAla--Leu 833
DB 2644 ACC-----ATGAGAGATGAGAGGACATCAACATCTGTAAACAACCTG 2685
QY 834 GlnIysLeuIleLeuGluAspCys-----GlyIleThrAlaThr 846
DB 2686 AAACCTTGAGTATTCATGACCTACAGATCAACGCTGCGGGTGTCTGACT----- 2739
QY 847 GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
DB 2740 -----GACGCTGGGTAACTTGAAGAACCTTCAACAAAGCTCAATAAG 2781
QY 867 SerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuPro 886
DB 2782 GATAACATTAAGATGAATGAAGAGATGCTATTAACCTGAGCTGAAGGCTGAAA----- 2835
QY 887 HisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGly 906
DB 2836 -----AACCTGAAGAGATGTGTTATTTCAT----- 2862
QY 907 PheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsn 926
DB 2863 -----TTGACCCCACTGTCT----- 2877
QY 927 ProValGluAsp-----AsnGlyValIysLeuLeuCysGluValMetArgGluProSer 944
DB 2878 -----GACATTGAGAGAGAGATGATTAACATGACAGCTCTCTCAAGTAAACCC 2928
QY 945 CysHisLeuGlnAspLeuGlnLeuValIysCysHisLeuThrAlaAlaCysCysGluSer 964
DB 2929 TGTGACCTTGAAGAAATTCATTAAGTCTCTGCTGCTGCTGCAATGCAATGCAATGCAATTC 2988
QY 965 LeuSerCysValIleSerArgSerArgHisLeuIysSerLeuAspLeuThrAspAsnAla 984
DB 2989 CTAGCTCAAGATCTTCACAAATTTGCTCAACCTGACAGCATTTCTGATTTACAGAAAATTAC 3048
QY 985 LeuGlyAspGlyGlyValAlaAlaLeuCysGlnGlyLeuIysGlnIysAsnSerVal--- 1003
DB 3049 CTGAAAAAAGATGAAATGAAGCTCTTCATGAACCTGATGACAGATGAAGTGAAGTGAAGA 3108
QY 1003 ----- 1003
DB 3109 CAGCTACCGCAGCTGATGCTGCTGGGGCTGTGACGTGCAAGGACGCTGAGCAGCCTG 3168
QY 1004 -----LeuThrArgLeuGlyLeuIysAlaAlaCysGlyLeu 1014
DB 3169 TTGAAACATTGAGAGAGAGTCCACACACTGCTGAGGTGTAATAAACTGAGAGACTC 3228
QY 1015 ThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsn-----ArgHisLeu 1032
DB 3229 ACGAGTACAGAGATTAGATTAGCTGATTTTGGAAAGAACCTCTGAAAACTTC 3288
QY 1033 ThrSerLeuAsnLeuValGlnAsnAsnPheSerProIysGlyMetMetIysLeuCysSer 1052
DB 3289 CAGCAGTGAATTTGGCGGGAATCGTGTGAGCAGATGATGATGCTTCCCTTCATGAGT 3348
QY 1053 AlaPheAlaCysProThrSerAsnLeuGlnIleGlyLeuTrpIysTrpIleIys--- 1071
DB 3349 GTATT-----GAGAACTCTTAAGCAATTAGTGTTTTGACTTAACTAA 3396
QY 1072 -----ProValGlnIleArgIysLeu----- 1078
DB 3397 GAATTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3456
QY 1079 ---LeuGlnGluValGlnLeuLeuIysProArgValValIleAspGlySerTrpHisSer 1097
DB 3457 TTTCTGCAAGAGAGTGAAGCTGCTGTT-----GGGTGG---CAA 3489

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QY 1098 PheAspGluAspAsp 1102
DB 3490 TTTGATGATGATGATGAT 3504

RESULT 13
US-11-145-631-12/c
; Sequence 12, Application US/11145631
; Publication No. US20060003409A1
GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/11/145, 631
; PRIOR FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: US/09/841, 739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697, 089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161, 822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 3615
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-631-12

Alignment Scores:
Pred. No.: 1,91e-14 Length: 3615
Score: 276.00 Matches: 254
Percent Similarity: 37.03% Conservative: 193
Best Local Similarity: 21.04% Mismatches: 423
Query Match: 3,90% Indels: 340
DB: 8 Gaps: 56

US-10-066-521-6 (1-1344) x US-11-145-631-12 (1-3615)
QY 17 CysLeuTrpGluLeuAspIysGlnGluPheGlnThrPheGlyLeuLeuIysIysIys 36
DB 3075 TGTGCGAAGAGGTGAGAGAGATGCTCTGAGGATCATTCATGATTTGAAAAAG 3016
QY 37 SerSerGluSerThrThrCysSerIleProGlnPheGlnIleGluAsnAlaAsnValGlu 56
DB 3015 GGTTCAGAGTCC-----TGTAACTC----- 2995
QY 57 CysLeuAlaLeuLeuHisGluTrpGlyAlaSerLeuAlaTrpAlaThrSerIle 76
DB 2994 -----TTTCTTAATCCCTTAAGAGAGTGG-----AACTAT 2965
QY 77 SerIlePheGluAsnMetAsnLeuArgThrLeuSerGluIysAlaArgAspAspMetIys 96
DB 2964 CCTTAATTCAGAGCTTGAATGAGACAAAGTTTGAAGAGACACAGAAATGGGCTCTTTT 2905
QY 97 IysIleSerGlnAlaMetGlnGlnGlnGlnGlnAlaThrAlaAlaGluThrGlnGlnGln 116
DB 2904 AACATCACTCTCTCTAATAGTCTTTTATCATGACATGACAGAGAGAGACTTGAGACAT 2845
QY 117 IleSerGlnAlaMetGlnGlnGlnGlnGlnAlaThrAlaAlaGluThrGlnGlnGln 136
DB 2844 TTGGCTCAGAGATTAAAGAGACTTGTACCAATCCCATCTTTTCTGAACCTTTATCCCTT 2785
QY 137 GlyGlyAspThrTrpAspTrpIysSerHisValMetThrIysPheAlaGluGluGluAsp 156
DB 2784 GGTGAAGATATT-----GACATTAATTTTAACTTGAAGACACTTCACAGAACTGTCTC 2728
QY 157 ValArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGly 176
DB 2727 TGGAGAGAGACCAACACATCAACCGCGAGAGAGCTGACCTGTAATGGCTCTCGAG 2668
QY 177 AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHisGlyIysSer 196
DB 2667 GCTCTTCAGAGC-----CCCTGCATCATTTGAAGGGAATCT 2632

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QY	197	GLYTLLEGLYSERIALALEUALARGRGLLEVALLEUCYSTPRALAGLNGLYLEU	216
DB	2631	GGCAAGGCAAGTCCACTGTCTCCAGGAATTCCTCTGGGGCTCCGAAAGTCC	2572
QY	217	TYRGLN---GLYMETPHESETYRVALPHEPHEUPROVALAGLUMETGLARGLYS	235
DB	2571	AAGGCTCGACCAATTCAAATTGCTCTTCTCCGTCCGTCCAGAGGCCAG-----	2518
QY	236	LYSGLUSESERVALTHRGHPHEILESERGLUTRPROAP-----	250
DB	2517	-----GGTGAACCTTTGAAACCTCTGTATCAACTCTGATATACCTGCAATACCTGCAATC	2464
QY	251	---SERGINALPROVALTHRGHILEMETERHGRPROGINAGLYLEUPHEILE	269
DB	2463	AGAAAGCAACATTCATCGCCATGCTGTGGAAGCTCGGCGAAGAGGTTCTTTCTTCTT	2404
QY	270	ASPGLYPHEASPRLEUGLYSERVALLEUAMHNPHTHLYSLEUCYLYASPTP	289
DB	2403	GATGGCTACATATGAATC-----AMGCCCAAGACTGCCAGAA-----	2365
QY	290	ALAGLIUSGLINPROPHETHTLEULIARGSERLEULEADGLYVALLEUENPRO	309
DB	2364	-----ATCAAGCCCTGATTAAGAAACCAACCCGCTTC	2332
QY	310	GLUSERPHEULILEVALTHR-----VALARGSPVALGLY	321
DB	2331	AAGAACATGTCATCTGTACCACTAACCACTAGTCCCTGAGGACATATCGGCAATTTGGT	2272
QY	322	THRGHLYSLEUYSERGLIYVALSERPROARGTYRLEULEUVALARGLYLSESR	341
DB	2271	GCC-----CTGACGCTGAGGCTGGGAGATATGACAGAAAGCAAGCGCCAGGCTCTCAT	2218
QY	342	GLYGLUGLARGILEHILEULEUSHENGULARGLYLLEGLIUNHSEGLIYSETHRGLN	361
DB	2217	CGAAGAGTCGATTAAGAGAGCTTCTGAAGCTTGTTCCTCAATTCAGAAATTCAGG	2158
QY	362	GLYLEUARGALILEMETASNAHARGGLIULEUENHARGINCYSGINVALPROALVAL	381
DB	2157	TGCTTGAAGAAATCTCATG-----AAGACCCCTCTCTCTT	2125
QY	382	GLYSERLEULIECYVALALEUENLEUENHNSPRVALVALIGLYUSERVALALAPRO	401
DB	2124	GTGCTCATCACTGTG---GCATCCAGATG-----GGGAAAGGAGATTCAC	2080
QY	402	PHEANGLINTHRLIETHRGLYLEUHIISALAPHEVALPHEHISGLINLEUTHRPROARG	421
DB	2079	TCTACACACAAACAAAGCTGTTCAT-----ACCTTCTATGATCTG-----	2038
QY	422	GLIYVALARGARGCYSELEUAMHENGULUGLARGVALVALLEULYSPARGPHECYARG	441
DB	2037	---TTGAATACAGAAAAACAAACACAAACATTAAGGTGTGGCTGCAAGTCACTTATTCGG	1981
QY	442	-----METALVALIGLIGLYVALITRPMARGLYSERVALPHE	454
DB	1980	AGCCTCGACCACTGTGAGACCTACTCTTGAGGAGTGCTTCCACAAAGTTGATTC	1921
QY	455	ASPGLYASPRLEUMETVALIGLNGLYLEUGLYUSERGLIULEUARGALALEUPHEHIS	474
DB	1920	GAACTGCAGAGAT-----GTGCCAGCGTGAATGAG-----	1891
QY	475	METANILILEULEUPROAPSERHISCYSGIUGLUTR-----	487
DB	1890	---GATGCTCTGCTACAACTGGGCTCTCTGTAAATATACAGCTCAAGGTTCAAGCCA	1834
QY	488	---TYRTHRPHEHISLEUSERLEUENHNSPRPHECYVALALALA-----LEUITYR	504
DB	1883	AAGTATAAATCTTTCAAGATCATTCACAGAGATACAGAGACGACGAAAGTCAAGAGT	1774
QY	505	VALLEUGLUGLYLEUGLILEGLUPROALALEUCYSPROLEUTYRVALIGLYSETHRILYS	524
DB	1773	TTATTGAAGCTTCATGAGCCAGAG-----GAGGTGACCAAG	1738

QY	525	ArgSerMetGluLeuLysGlnAlaGlyPheHis-----IleHis-SerLeuThr	540
Db	1737	GGGATGAGTACTTCGCAGAAAAT--GGTTTCATTTCCAGATTCATCATCCATTATAGCAG	1678
QY	540	PMetLysArgPheLeuPheGlyLeuValSerGlyLysArgArgProLeuGluValLe	560
Db	1678	CCTGCTCCGGTACACCTTGAGTACTCTGTGGAAAGCCACACAGGGCTGTATTACACACTT	1611
QY	560	uLeu-----GlyCysProValProLeuGlyValLysGlnLysLeuLysIle	575
Db	1618	CGACGACAGTATCAACACAGCGGTGCTTCTCGCATTTTCATTCGCCAAGAGCGCTTC--	1561
QY	575	sTrpValSerLeuLeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAl	595
Db	1560	-TGGAGACAGAAATCTTTGCAAAAGTGTGMAAAACACCTAGACGAATAATTTGAAAGC	1507
QY	595	aPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPh	615
Db	1501	CATTAATCAATC-----AATTCTTTGTGAGTGGAGTGCATCATTTATATA	1466
QY	615	eGlnGlu-ValTrp-----LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerP	633
Db	1459	TCARAGAGTATACATCCAAATACAGCCCTGAGCCAAAGAAATTTGAAGCTT-----TCTT	1400
QY	633	heCysLeuGlnIleCysProGlyLeuArgLysLysIleArgValAspValLysGlyIlePheP	653
Db	1408	TCAAAGGTA-----AAAGCTTATATATCAACTCAGGGAAACATCCC	1370
QY	653	roArgAsp-----GluSerAlaGluAlaCysProValVal-----	664
Db	1369	CGATTACTTATTTGACTCTTTTGAACATTTTGCCCAATGTGTGCAAGTCCCTGGACTTCAT	1311
QY	665	-----ProLeuTrpMetArgAspLysThrLeuIleGlnGlnGln-	677
Db	1309	TAAATGCACTTTTATGGGGGAGCTATGGCTTCATGGGAAAAGCTGCAGAAAGACACAGG	1255
QY	678	TrpGluAspPheCysSerMetLeuGlyThrHisProGlnIleuArgGlnLeuAspLeuGly	697
Db	1249	TGG-----AATCCACAT-----	1238
QY	698	SerSerIleLeuThrGluArgAlaMetLysThrLeuGlyValAlaLysLeuArgHisProThr	717
Db	1237	-----GAAAGAGGCCCCAGAAACCTTACATCCACAG-----	1200
QY	718	CysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnIleLysLeu	737
Db	1207	-----CAGGGCTGATCTTT--GTCTTCAACAGGAAGCAAGATTCAGCA--CTC	1165
QY	738	TrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLysLeu	757
Db	1160	TGGAGGTC--ACACTC-----CGGAGATTCAGCAAGATTGAAAT-----	1120
QY	758	LysGlnGluAspValArgMetAlaCysGlnAlaLysLysHisProLysCysLysLeuGlu	777
Db	1135	--AAGCAAGATATGAGATATCTGGGAGAAATATTCAGCTC-----GCCACA	1081
QY	778	SerLeuArgLeuAsp-----CysCysGlyLeuThrHisAlaCysArgLeuLysIle	794
Db	1080	AGCCTCAGGCTCAAAATAAGAGATGTGCTGTGTGCGCTGAGAC-----CTC	1033
QY	795	SerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysVal	814
Db	1032	ACTTTGGTCTCAGCAGCCTGTGAAGAACTTTATCTTCATGATGATGAGCCAGTCCCTCC	973
QY	815	ThrArgGlnGlyValMetProLeuSerIleAspAlaLeuArgValSerGlnCysAla---Leu	833
Db	972	ACC-----ATAGAAATGAGAGGACATCATCATCTGTAACAACCTGG	931
QY	834	GlnLysLeuIleLeuGluAspCys-----GlyIleThrAlaThr	846
Db	930	AAAACCTTGAGTATTCATGACCTTACAGAAATCAACAGCGCTCCGGGTGTGTACT--	877
QY	847	GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLysCysLeu	866

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Db 876 -----GACAGCTTGGTAACTTGAAGAACTTACAACTCATATG 835
Qy 867 SerhansSerLeuGlyAsnGlyValAsnLeuLeuCybArgSerMetArgLeuPro 886
Db 834 GATAAATTAAGATGAATGAAGATGCTATTAAGAACTAGTGAAGCGCTGAAA----- 781
Qy 887 HisCySerLeuGlnArgLeuMetLeuAsnGlnCybHisLeuAspThrAlaGlyCybGly 906
Db 780 -----AACCTGAAGAGATGTTATTTTCAT----- 754
Qy 907 PheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsn 926
Db 753 -----TTGACCACTTCTCT----- 739
Qy 927 ProValGluAsp-----AsnGlyValIyLeuLeuLeuCybGluValMetArgGluProSer 944
Db 738 -----GACATTTGAGAGGGAATGATGATTAACATAGCAAGTCTCTCAAGTGAACCC 688
Qy 945 CybHisLeuGlnAspLeuGlnLeuValIyCybHisLeuThrAlaAlaCybCybGluSer 964
Db 687 TGTAACTTGAAGAAATTCATTAAGTCTCTGCTGCTGCTGCTGCAATGCAAGTGAATTC 628
Qy 965 LeuSerCybValIleSerArgSerArgHisLeuIySerLeuAspLeuThrAspAsnAla 984
Db 627 CTAGCTGAGATCTTCAACAATTTGGTCAAACTGAGCATCTTGTATTTCAAGAAATTAAC 568
Qy 985 LeuGlyAspGlyGlyValAlaAlaLeuCybGluGlyLeuIyGlnIyAsnSerVal--- 1003
Db 567 CTGGAAGAAAGATGAATGAAGCTCTTCATGAATGATGACAGATGAAGATGAGTCTGTA 508
Qy 1003 ----- 1003
Db 507 CAGCTACCGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
Qy 1004 -----LeuThrArgLeuGlyLeuIyAlaCybGlyLeu 1014
Db 447 TTGAAACATTTGGAGAGAGTCCCAACAATCTGCAAGCTTGGTTGAAAACGAGACTC 388
Qy 1015 ThrSerAspCybCybGluAlaLeuSerLeuAlaLeuSerCybAsn-----ArgHisLeu 1032
Db 387 ACAAGTACAGAGATTAAGATTTAGTGCATTTTGGAAAGAACCTCTGTAAGAACTTC 328
Qy 1033 ThrSerLeuAsnLeuValGlnAsnAsnPheSerProIyGlyMetMetIyLeuCybSer 1052
Db 327 CAGCAGTGAATTTGGCGGGAATGCTGTGAGCAGTGAATGATGCTGCTGCTGCTGCTG 268
Qy 1053 AlaPheAlaCybProThrSerAsnLeuGlnIleGlyLeuTrpIyGlnIy--- 1071
Db 267 GTATTT-----GAGAACTTAAAGCAATTAAGCTTTTGGACTTTAGTACTAA 220
Qy 1072 -----ProValGlnIleArgIyLeu----- 1078
Db 219 GAATTTCTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 160
Qy 1079 ---LeuGluGluValGlnLeuLeuIyProArgValIleAspGlySerTrpHisSer 1097
Db 159 TTTTGCAGAGAGCTAGGCTTGT-----GGGTGG---CAA 127
Qy 1098 PheAspGluAspAsp 1102
Db 126 TTTGATGATGATGAT 112

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RESULT 14
US-11-128-061-276
; Sequence 276, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.

```

```

; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128, 061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 276
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (363)..(379)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-276

Alignment Scores:
Pred. No.: 3.08e-15 Length: 536
Score: 270.00 Matches: 64
Percent Similarity: 50.00% Conservative: 30
Best Local Similarity: 34.04% Mismatches: 66
Query Match: 3.82% Indels: 28
DB: 8 Gaps: 4

US-10-066-521-6 (1-1344) x US-11-128-061-276 (1-536)

Qy 779 LeuArgLeuAspCybCybGlyLeuThrHisAlaCybTrpLeuIyIleSerGlnIleLeu 798
Db 45 CTCAGATTACACTG----- 59
Qy 799 ThrThrSerProSerLeuIySerLeuSerLeuAlaGlyAsnIyValThrAsp----- 816
Db 60 -----GCACCCACATG---AGTCTTGAACATCCAKTGTGAGCAGTGAATGATCCAGG 110
Qy 817 ---GlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCybAlaLeuGlnIy 835
Db 111 TGACAGAGACTCTCTCCCTGATCCAGCAATACCAAGTGTCAAG----- 155
Qy 836 LeuIleLeuGluAspCybGlyIleThrAlaThrGlyCybGlnSerLeuAlaSerAlaLeu 855
Db 156 -----TTGAGTGAAGTGTGTCTCACTAGAGTCCGCTCAAGACATCACTCAACCAATT 209
Qy 856 ValSerAsnArgSerLeuThrHisLeuCybLeuSerAsnAsnSerLeuGlyAsnGly 875
Db 210 CAGTCAACCCCACTTAACAGAGCTCAGCTTAAGCAACATGAGCTGGGGGACCTGCG 269
Qy 876 ValAsnLeuLeuCybArgSerMetArgLeuProHisCybSerLeuGlnArgLeuMetLeu 895
Db 270 GTGTGCTGTGAACTTCCAGGCGCTGCAAGATCCCACTTAAGATCAGAGATGAGCTG 329
Qy 896 AsnGlnCybHisLeuAspThrAlaGlyCybGlyPheLeuAlaLeuAlaLeuMetGlyAsn 915
Db 330 CAGATTGCACTTGAACCGAGCGCTGTGTGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNN 389
Qy 916 SerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIyLeu 935
Db 390 CCTACCTCGCGGAGACTACATCTCACTGATTAATCTCTCGGAGATGACAGTCTGAAGCTG 449
Qy 936 LeuCybGluValMetArgGluProSerCybHisLeuGlnAspLeuGlnLeuValIyCyb 955
Db 450 CTCTGTGAAGACTCTTGAACCCCAATGCGCGCTTGAAGACTTCAAGTGAATATATCTGT 509
Qy 956 HisLeuThrAlaAlaCybCybGlu 963
Db 510 AACCTCAAGACTTACCAAGTTGCGAG 533

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RESULT 15

US-11-128-061-3918  
Sequence 3918, Application US/11128061  
Publication No. US20060003958A1  
GENERAL INFORMATION:  
APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Hann, Louane E.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
FILE REFERENCE: 01997.027701  
CURRENT APPLICATION NUMBER: US/11/128,061  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 3918  
LENGTH: 536  
TYPE: DNA  
ORGANISM: Cricetus griseus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (363)..(379)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-128-061-3918

Alignment Scores:  
Pred. No.: 3,08e-15 Length: 536  
Score: 270.00 Matches: 64  
Percent Similarity: 50.00% Conservative: 30  
Best Local Similarity: 34.04% Mismatches: 66  
Query Match: 3.82% Indels: 28  
DB: 8 Gaps: 4

US-10-066-521-6 (1-1344) x US-11-128-061-3918 (1-536)

QY 779 leuArgleuAProSerCySgIleuThrHisAlaCySfYleuYsIleSerGlnIleleu 798  
DB 45 CTGAGATTACACTGT----- 59  
QY 799 ThrThrSerProSerleuYsSerleuSerleuAlaGlyAsnYsValThrAsp----- 816  
DB 60 -----GCACCCACCATG--AGTCTTGACATCCATGTCGAGCAGTGAATGCCAGG 110  
QY 817 ---GlnGlyValMetProLeuSerAspAlaIleuArgValSerGlnCySAlaIleuGlnYs 835  
DB 111 TGGACAGAGCTCTTCCCTGATCCAGCAATACCAAGTGTGCAG----- 155  
QY 836 leuIleleuGluAProCySgIYleThrAlaThrGlyCySgInSerleuAlaSerAlaIleu 855  
DB 156 -----TTGGATGACTGTGTCTCAGTGGGTGCGGTGCAAGAATCAGCTCAKCCATT 209  
QY 856 ValSerSerArgSerleuThrHisIleuCySleuSerSerAsnSerleuGlyAsnGlnGly 875  
DB 210 CAGTCCAAACCCCTTAACAGACTCAGCTATGCAACAAATGAGCTGGGGACCTGGC 269  
QY 876 ValAsnleuLeuCySArgSerMetArgleuProHisCySserleuGlnArgleuMetleu 895  
DB 270 GTGTGCTGTGAATCCASGGCTGACAGATCCACCTGAAGTCAAGAGCTAAGCTG 329  
QY 896 AsnGlnCySHisIleuAProThrAlaGlyCySgIYPheleuAlaIleuAlaIleuMetGlyAsn 915  
DB 330 CAGATGACAGCTTGAACGAGCTGCTGAGNNNNNNNNNNNNNNNNNNNNNACTTCTT 389  
QY 916 SerTrpIleuThrHisIleuSerleuSerMetAsnProValGluAProAsnGlyValIleu 935  
DB 390 CTAACCTGGGAGGAGTAACTCAATCTCAGTGAATATCTCTGGAGATGACAGTCTGAAGCTG 449

QY 936 leuCySgIuValMetArgGluProSerCySHisIleuGlnAProleuGluIleuValYsCyS 955  
DB 450 CTCTGTGAAGACTTCTGACACCCCAATGCGGCTTGAGAAAGCTTCAGTTGGAATACTGT 509  
QY 956 HisIleuThrAlaAlaCySgIu 963  
DB 510 AACCTCAGACTTACCAAGTTGCCAG 533

Search completed: January 21, 2006, 13:04:31  
Job time : 531 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

# OM protein - nucleic search, using frame\_p2n model

Run on: January 21, 2006, 05:50:17 ; Search time 2275 Seconds  
(without alignments)  
4885,294 Million cell updates/sec

Title: US-10-066-521-6  
Perfect score: 7074  
Sequence: 1 MEGXSLTPSXYGLQKLYE.....DDHSGVMSLGAAGLEIVS 1344

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues  
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=x1h  
-Q=/cgn2\_1/USPRO.epool/US10066521/runat 20012006.145900.21102/app\_query.fasta.1.1543  
-DB=Published Applications NA Main -QFMT=fastcap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext  
-HEA=516500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10066521@cgn 1.1.1594 @runat 20012006.145900.21102 -NCPU=6 -ICPU=3  
-NO MAP -LARGESQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=10 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : Published Applications NA Main:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7074	100.0	4035	US-10-124-498-5	Sequence 5, Appli
2	7074	100.0	4035	US-10-066-521-5	Sequence 3, Appli
3	5756	81.4	3489	US-10-416-642-3	Sequence 3, Appli
4	5756	81.4	3926	US-10-216-645-1	Sequence 1, Appli
5	5741.5	81.2	3885	US-10-860-761-3	Sequence 3, Appli
6	5741.5	81.2	3900	US-10-399-443-23	Sequence 23, Appli
7	5741.5	81.2	3900	US-10-677-943-23	Sequence 23, Appli

8	5683.5	80.3	3830	US-10-216-645-3	Sequence 3, Appli
9	5120	72.4	3226	US-10-092-900A-347	Sequence 347, App
10	2688	38.0	3447	US-10-399-443-5	Sequence 5, Appli
11	2688	38.0	3447	US-10-677-943-5	Sequence 5, Appli
12	2005	28.3	1157	US-10-399-443-1	Sequence 1, Appli
13	2005	28.3	1157	US-10-677-943-1	Sequence 1, Appli
14	1885.5	26.7	3521	US-10-794-342-2	Sequence 2, Appli
15	1435	20.3	3368	US-10-124-498-23	Sequence 23, Appli
16	1435	20.3	3368	US-10-066-521-23	Sequence 23, Appli
17	1434	20.3	2982	US-10-124-498-25	Sequence 25, Appli
18	1434	20.3	2982	US-10-066-521-25	Sequence 25, Appli
19	1434	20.3	2985	US-09-965-621-15	Sequence 15, Appli
20	1434	20.3	2985	US-10-407-866-15	Sequence 15, Appli
21	1434	20.3	2985	US-10-781-294-15	Sequence 15, Appli
22	1402	19.8	2775	US-10-357-820-51	Sequence 51, Appli
23	1335	18.9	1075	US-10-399-443-3	Sequence 3, Appli
24	1335	18.9	1075	US-10-677-943-3	Sequence 3, Appli
25	1332.5	18.8	3484	US-10-794-342-3	Sequence 3, Appli
26	1320.5	18.7	3108	US-09-965-621-23	Sequence 23, Appli
27	1320.5	18.7	3108	US-10-407-866-23	Sequence 23, Appli
28	1320.5	18.7	3108	US-10-781-294-23	Sequence 23, Appli
29	1315.5	18.6	3190	US-10-094-749-1079	Sequence 1079, Ap
30	1315.5	18.6	3172	US-10-399-037-74	Sequence 74, Appli
31	1314.5	18.6	2883	US-10-161-493-3	Sequence 3, Appli
32	1313.5	18.6	3540	US-10-794-342-7	Sequence 7, Appli
33	1304.5	18.4	3218	US-10-407-866-67	Sequence 67, Appli
34	1303.5	18.4	3186	US-10-124-498-17	Sequence 17, Appli
35	1303.5	18.4	3186	US-10-066-521-17	Sequence 17, Appli
36	1289.5	18.2	2575	US-09-848-035-7	Sequence 7, Appli
37	1289.5	18.2	2575	US-09-986-224-7	Sequence 7, Appli
38	1289.5	18.2	2575	US-10-116-422-7	Sequence 7, Appli
39	1255	17.7	3102	US-10-127-516-6	Sequence 6, Appli
40	1255	17.7	3102	US-10-027-629-6	Sequence 6, Appli
41	1255	17.7	3102	US-10-132-967-6	Sequence 6, Appli
42	1255	17.7	3857	US-10-127-516-4	Sequence 4, Appli
43	1255	17.7	3857	US-10-027-629-4	Sequence 4, Appli
44	1255	17.7	3857	US-10-132-967-4	Sequence 4, Appli
45	1250.5	17.7	3531	US-10-756-149-3252	Sequence 3252, Ap

## ALIGNMENTS

RESULT 1  
US-10-124-498-5  
; Sequence 5, Application US/10124498  
; Publication No. US20030017983A1  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; APPLICANT: Wang, Weiye  
; APPLICANT: Blatcher, Maria  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR  
; FILE REFERENCE: 07334-367001  
; CURRENT APPLICATION NUMBER: US/10/124,498  
; CURRENT FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 10/066,521  
; PRIOR FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/318,645  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/265,231  
; PRIOR FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 4035  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(4032)  
; US-10-124-498-5

Alignment Scores:

Pred. No.: 0 Length: 4035  
 Score: 7074.00 Matches: 1344  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-124-498-5 (1-4035)

QY 1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGluIleuGluIleuTyrGlu 20  
 DB 1 ATGAGAAAGAGCAAAATGCTCACCCTTTCCAGCTACGAGCTGCAATGCTCTAAGAG 60  
 QY 21 LeuAspLysGluGluPheGluIleuThrPheLysGluLeuLeuLysLysSerSerGluSer 40  
 DB 61 CTAGACAGAGAAAGATTTCAGACATTCAAGAAATTCTAAAGAAAGAAATCTTCGAATCG 120  
 QY 41 ThrThrCysSerIleProGluIleuGluIleuGluIleuValIleuValIleuValIleu 60  
 DB 121 ACCACATGCTCTATTCCACAGTTTGAATCGAAGATCCCAACGTGGAATGCTGGCACTC 180  
 QY 61 LeuLeuHisGluIleuTyrGluValIleuSerLeuValIleuThrIleuSerIleuPheGlu 80  
 DB 181 CTCTTGATAGATATTAATGAGACATCGCTGAGCTGAGCTCATTAAGCATCTTGAA 240  
 QY 81 AsnMetAsnLeuArgThrLeuSerGluLysIleuArgAspAspMetLysIleuSerGlu 100  
 DB 241 AACATGAACCTGCGAACCTCTCGAGAGAGCAAGGATGACATGAAAAAATTTCCAA 300  
 QY 101 AlaMetGluGluGluIleuValIleuThrAlaIleuGluIleuGluIleuIleuSerGlu 120  
 DB 301 GCTTGTGAAACAAAGAGTGCACAGCAGCAGACAGACAAAGAAATTTCCAAAGCT 360  
 QY 121 MetGluGluGluGluValIleuThrAlaIleuGluIleuGluIleuGluIleuValIleu 140  
 DB 361 ATGGAACAAAGAGTGCACAGCAGCAGACAGACAAAGAAATTTCCAAAGCT 420  
 QY 141 TrpAspTyrLysSerHisValMetThrLysPheAlaGluGluIleuAspValIleuArgSer 160  
 DB 421 TGGGACATCAAGAGTGCACAGTGAATTCGCTGAGAGAGAGATGATACGTGATAGT 480  
 QY 161 PheGluIleuThrAlaIleuAspTyrProGluMetGluIleuValIleuValIleuPheAsp 180  
 DB 481 TTTGAAACAACTGCTGCTGACCTGCGCGAAATGCAAACTGCTGCTTTGATTC 540  
 QY 181 AspArgTrpGlyPheArgProArgThrValIleuHisGluLysSerGlyIleuGlyLys 200  
 DB 541 GACCGGTGGGCTTCGCGCTCGCAGCGAGTGTGACGGAAGTCAAGAAATTTGGAAA 600  
 QY 201 SerAlaLeuValIleuArgIleuValIleuCysTrpAlaGluIleuGlyIleuTyrGluIleu 220  
 DB 601 TCGGCTCTTACGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 QY 221 PheSerTyrValPhePheLeuProValIleuGluMetGluIleuGlyLysSerSerVal 240  
 DB 661 TTTCTCCATCACT 720  
 QY 241 ThrGluIleuIleuSerArgIleuTyrProAspSerGluIleuProValIleuThrIleuMetSer 260  
 DB 721 ACAGAGTTCATCTCAGAGAGTGCACAGCTCCAGAGCTCGGAGTCAAGATATATGCTC 780  
 QY 261 ArgProGluIleuArgLeuPheIleuIleuAspGlyPheAspAspLeuGlySerValIleuAsn 280  
 DB 781 CGACCAAAAGGCTGTTGTTTCATTTGACGCTTTCATGACCTGCTGCTGCTGCTGCT 840  
 QY 281 AsnAspThrIleuLysCysLysAspTyrAlaGluLysGluIleuProPheThrIleuIleuArg 300  
 DB 841 AATGACCAAAAGCTCTGCAAGAGCTGAGAGAGAGAGCTCTGCTTCAACCTCATACGC 900  
 QY 301 SerLeuLeuArgLysValIleuLeuProGluSerPheLeuIleuValIleuThrAlaArgAspVal 320  
 DB 901 AGTTCCTGAGAGAGTCTGCTCTGATGATCTTCTGATGATGATGATGATGATGATGATG 960

QY 321 GlyThrGluLysLeuLysSerGluValIleuSerProArgTyrLeuLeuValIleuGlyIle 340  
 DB 961 GGCAAGAGAGAGCTCAAGTCAAGAGTGTCTCCCGCTTACCTGTTAGTAGAGGAAATC 1020  
 QY 341 SerGlyGluIleuArgIleuIleuLeuLeuGluIleuGlyIleuGlyIleuHisGluIleuThr 360  
 DB 1021 TCGGGGAAACAAAGAAATCCATGCTCTGAGCGCGAGATGAGTGAAGATCAAGAAACA 1080  
 QY 361 GlnGlyLeuArgAlaIleuMetAsnAsnArgGluLeuLeuAspGlnCysGlnValIleuProAla 380  
 DB 1081 CAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 QY 381 ValGlySerLeuIleuCysValIleuGluIleuGluIleuAspValIleuGlyIleuSerValIleu 400  
 DB 1141 GTGGGCTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
 QY 401 ProPheAsnGlnIleuThrIleuThrGlyLeuHisAlaIleuPheValIleuThrPro 420  
 DB 1201 CCTTCAACCAACAGCTCAAGAGCTGACAGCGCTTTGTGTTCATTCAGCTCACCCCT 1260  
 QY 421 ArgGlyValIleuArgArgCysLeuAsnLeuGluIleuArgValIleuLeuLysArgPheCys 440  
 DB 1261 CGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 QY 441 ArgMetAlaValIleuGluValIleuProAsnArgLysSerValIleuAspGlyAspAspLeuMet 460  
 DB 1321 CGTATGCTGTGAGAGGAGTGTGAATAGGAATGAGTGTGTTGATGTGACGACCTCATG 1380  
 QY 461 ValGluIleuIleuGlyIleuSerGluLeuArgAlaIleuPheHisMetAsnIleuLeuPro 480  
 DB 1381 GTTCAGAGACTCGGGAGTGTGAGCTCGTGTCTGTTCATGAAACATCTCTTCCCA 1440  
 QY 481 AspSerHisCysGluGluIleuTyrThrPhePheHisLeuSerLeuGluIleuAspPheCysAla 500  
 DB 1441 GACAGCCTGCTGAGAGATCACTACCTTCTTCACTGATCTCCAGACCTTCTGTGCC 1500  
 QY 501 AlaLeuTyrTyrValIleuGluIleuGluIleuGluIleuProAlaLeuCysProLeuTyrVal 520  
 DB 1501 GCCTTGTATCACTGTTAGAGGCTGGAATGAGCACTGCTGCTGCTGCTGCTGCTGCTG 1560  
 QY 521 GluLysThrLysArgSerMetGluLeuLysGluAlaGlyPheHisIleuHisSerLeuTyr 540  
 DB 1561 GAGAAACAAAGAGTGCATGAGCTTAAACAGAGGCTTCCATATCCACTGCTTTGG 1620  
 QY 541 MetLysArgPheLeuPheGlyLeuValIleuSerGluAspValIleuArgArgProLeuGluValIleu 560  
 DB 1621 ATGAGGCTTCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 QY 561 LeuGlyCysProValIleuLeuGlyValIleuGluLysLeuLeuHisTyrValIleuSerLeu 580  
 DB 1681 CTGGGCTGTCCCGTCCCTGCGGGGTGAAACAGAACTTCTGCACTGGGCTCTCTGTTG 1740  
 QY 581 GlyGluIleuProAsnAlaThrThrProGlyAspThrIleuAspAlaPheHisCysLeuPhe 600  
 DB 1741 GGTGAGAGCTTATGCAACACCCAGAGAACCTCTGAGAGCTTCCACTGCTCTTTTC 1800  
 QY 601 GlnThrGluIleuAspLysGluPheValIleuArgLeuAlaLeuAsnSerPheGlnGluValIleu 620  
 DB 1801 GAGACTCAAGCAAAAGATTTGCTTGGCTTGGCATTAACGCTTCCAAAGAGTGTGCTT 1860  
 QY 621 ProIleuAsnGluLeuAspLeuIleuAspSerPheCysLeuGluIleuHisCysProTyr 640  
 DB 1861 CCGATTAAACCAAGAACTTGATGATCTTCTCTGCTTCCGCTCCGACCTGCTGCTAT 1920  
 QY 641 LeuArgLysIleuArgValIleuValIleuGlyIleuPheProArgAspGlyIleuValIleu 660  
 DB 1921 TTGGGAAATTTGGGAGTGTCAAAAGGATCTTCCAAAGATGATGCTGCTGAGGCA 1980  
 QY 661 CysProValIleuProLeuTyrMetArgAspLysThrLeuIleuGluIleuGluIleuTyrGluAsp 680  
 DB 1981 TGTCTGTGCTCTCTATGAGAGCGGAGATGAAGCTCTTATGAGAGAGTGGAGAT 2040  
 QY 681 PheCysSerMetLeuGlyIleuHisProHisLeuArgGluIleuAspLeuGlySerSerIle 700

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Db      2041 TTCTGCTCCATGCTTGGACCCACCACTGGCGGAGCTGGACCTGGGAGAGCATC 2100
Qy      701  LeuThrGluArgAlaMetLysThrLeuCyValAlaLysLeuArgH1SerProThyCysLysIle 720
Db      2101 CTGACAGAGCGGGGCGATGAAAGACCTGTGTGCGCAAGCTGAGGCAATCCCACTGGCAAGATA 2160
Qy      721  GluThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnH1SerLeuTrpArgIle 740
Db      2161 CAGACCTGATGTTTAAAGATGACAGATTACCCCTGGTGTGCGACCACTTGTGAGAAATC 2220
Qy      741  ValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrH1SerLeuGlyGlu 760
Db      2221 GTCATGGCCCAACCGTAACCTTAAGATCCCTCAACTGGGAGGCAACCACTGAAAGAAAG 2280
Qy      761  AspValArgMetAlaCysGlyValAlaLeuLysH1SerProLysCysLeuLeuGlySerLeuArg 780
Db      2281 GATGTAAAGATGGGGGTGTAAGCCTTAAACCAACCAAAATGTTGTGAGATCTTTGAGG 2340
Qy      781  LeuAspCysCysGlyLeuThrH1AlaCysTyrLeuLysIleSerGlnIleLeuThrThr 800
Db      2341 CTGATTTGCTGTGATGATGACCAATGCTCTTAACTTGAAGATCTCCAAATCTCTTAACAGC 2400
Qy      801  SerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMet 820
Db      2401 TCCCCAGCGCTGAATCTCTGAGCCTGGCAGAAACAAAGTGACAGACCAAGGAGTAATG 2460
Qy      821  ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAsp 840
Db      2461 CCTCTCAGTATGCTTGAAGAGTCTCCAGTGGCCCTGCAAGAGCTGATCTGAGAGAC 2520
Qy      841  CysGlyIleThrAlaThrGlyCysGlySerLeuAlaSerAlaLeuValSerAsnArgSer 860
Db      2521 TGTGGCATCACAGCCAGGGTTCGCAAGTCTGGCCTCAGCCCTGTGTGACAGACCGAGC 2580
Qy      861  LeuThrH1SerLeuCysLeuSerAsnAsnSerLeuGlyAsnGlyValAlaAsnLeuLys 880
Db      2581 TTGACACACCTGTGCTATTCACACACAGCTGGGGAAACAAAGGTGAATCTACTGTGT 2640
Qy      881  ArgSerMetArgLeuProH1CysSerLeuGlnArgLeuMetLeuAsnGlnCysH1Ser 900
Db      2641 CGATCCATGAGGCTTCCCACTGAGTGTGCAAGGCTGATGCTGAACCACTGACCACTG 2700
Qy      901  AspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThrH1S 920
Db      2701 GACACGGCTGAGCTGTGTTTCTTGTCACTTGGCTTATGAGTAACTCAATGCTAAGCAG 2760
Qy      921  LeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGlyValMet 940
Db      2761 CTGAGCCTTAGCAAGAACCTGTGGAAGACAAATGGCCGTGAAGCTTCTGTGCGAGGTATG 2820
Qy      941  ArgGluProSerCysH1SerLeuGlnAspLeuGluValLysCysH1SerLeuThrAla 960
Db      2821 AGAAGAACCATCTTGTCACTCTCAGAGACCTGAGATGTGTAAAGTGCATCTCAACGCCCG 2880
Qy      961  CysCysGlySerLeuSerCysValIleSerArgSerArgH1SerLeuSerLeuAspLeu 980
Db      2881 TGTCTGTAGAGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940
Qy      981  ThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlyGlyLeuLysGlnLys 1000
Db      2941 ACGGACCAATGCGCTGGGGTGAACGGTGGGGTCTGTGCTGTGCGAGGAGCTGAAGCAAA 3000
Qy      1001  AsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCysGlyGlu 1020
Db      3001 AACAGTGTCTGACAGAGACTGGGGTGAAGCACTGTGACCTTGATTCGATTCGTGTAG 3060
Qy      1021  AlaLeuSerLeuAlaLeuSerCysAsnArgH1SerLeuThrSerLeuAsnLeuValGlnAsn 1040
Db      3061 GCACCTTCTTGGCCCTTCTCTGCAACCGGCAATCTGACCAAGCTTAAACCTGGTGCAGAT 3120
Qy      1041  AsnAspSerProLysGlyMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsn 1060

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Db      3121 AACTCAGTCCCAAGAAAGATGATGACCTGTGTGCGCTTGTGCTGCCCTCCACCTTAAC 3180
Qy      1061  LeuGlnIleIleGlyLeuLeuTrpLysTrpGlnTyrProValGlnIleArgLysLeuLeuGlu 1080
Db      3181 TTACAGATTAATTGGGCTGTGGAAATGGCAGATACCTCTGTGCAAAATAGAAAGCTGTGAG 3240
Qy      1081  GluValGlnLeuLeuLysProArgValValIleAspGlySerTrpH1SerPheAspGlu 1100
Db      3241 GAATGCAAGCTACTCAAGCCCGGAGTGTGATTAATGACGATGATGAGTGTGCAATCTTTGATGA 3300
Qy      1101  AspAspArgH1SerLysIleGlyLeuThrPheArgLeuProGlySerArgAlaTrpProCys 1120
Db      3301 GATGACCGACCAAAATAGACTTAATCTTCCGCTCCCTGAAGACCGGGCAATGCGCATGT 3360
Qy      1121  AlaLeuLeuTrpGlyMetAsnProGlyGlnLysLysAspArgValSerLeuLeuAlaGlyAsp 1140
Db      3361 GCTTGTGCTGTGGGATGAAACCCAGAGCAGAAAGAGCTGTGTGTGCTTCTGTGGAGAC 3420
Qy      1141  PheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGlyGluSer 1160
Db      3421 TTCAAGAGCAGATACACGATTTGCCAAGTCTCTGCTGCGCCAGCGCAAAATGTGATGCC 3480
Qy      1161  GluArgValAspAsnValGluGlnSerSerProGlnProMetAlaGlyThrGluH1Lys 1180
Db      3481 CAGAGAGTTGACAAAGTGAGACAGAGCTCCCGCAACCACTGAGGACGCAACAA 3540
Qy      1181  GluAspLysMetLeuSerValGlyTyrSerGlyAlaTrpSerGluThrAlaGlyLeuGlu 1200
Db      3541 CAAGTAAATATGTTGATGTTGATATTCGGAAGCTGTGTGAAACGTCTGAGCTGAA 3600
Qy      1201  GlyLeuGlySerAsnSerAlaAspH1AspH1AspGlyMetAlaTrpSerLeuGlyArg 1220
Db      3601 GGGCTTGATCCAAAGTGATCATGACCAAGAGGTATGCGTGGTCACTGAGGAGAG 3660
Qy      1221  GluLeuSerSerArgGlyLeuCysProThrValLeuMetThrThrAlaValCysProGly 1240
Db      3661 GAGCTGAGCTCGAGGGCTGTGTGCCAAAGTGTGATGACCAAGCGGTGTGTCTGTGT 3720
Qy      1241  HisTrpGluArgLeuGlySerArgGlyTyrCysLeuAsnSerAlaAspAspH1SerGly 1260
Db      3721 CACTGGAGCGGCTGTGGGCTCTAGGGGCTGTGTCTTAAAGTCTGATGACCAAGCGGT 3780
Qy      1261  ValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSerAlaAspAsp 1280
Db      3781 GTGTCTGTGTCACAGGAGCGGCTGGGCTCGAGGGGCTTGTGTCAACAGCTGATGAC 3840
Qy      1281  HisSerGlyValAlaAlaTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuValSerAsnSer 1300
Db      3841 CACAGCGGTGTGGCTGTCACTGGAGCGGCTGGGCTCGAGGGGCTTGTGTCAACAGT 3900
Qy      1301  AlaAspAspH1SerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGluGlyLeuVal 1320
Db      3901 GCTATGACCAACAGCGGTGTCTGTGCTGATCTGGAGCGGCTGTGGGCTTGTGAGGGGCTTGTG 3960
Qy      1321  SerAsnSerAlaAspAspH1SerGlyValSerTrpSerLeuGlyAlaAlaGlyLeuGlu 1340
Db      3961 TCCAACAGTGTGATGACCAACAGCGGTGTGTCTGTGCTGAGGAGCGGCTGGGCTGAG 4020
Qy      1341  GlyLeuValSer 1344
Db      4021 GGGCTGTGTGTCT 4032

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## RESULT 2

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US-10-066-521-5
; Sequence 5, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Mang, Weiye
; APPLICANT: Blacher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; FILE REFERENCE: 07334-334001

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QY 601 GlnThrGlnAspLysGlnPheValArgLeuAlaLeuAsnSerPheGlnGluValTyrLeu 620  
 DB 1801 GAGCTCAAGCAAGAGCTTGTCTGCTGGCACTTAAACAGCTTCAAGAGGTGGCTT 1860  
 QY 621 ProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyr 640  
 DB 1861 CCGATTAACTGAGAACTGAGCTTGTATAGCATCTTCTGCTCTCAAGACAGCTGCTCGTAT 1920  
 QY 641 LeuArgLysIleArgValAspValIleGluIlePheProArgAsnGlnSerAlaGlnAla 660  
 DB 1921 TTGGGAAATTCGGGTGATGTCMAAGGATCTTCCAAAGAGATCCGCTGAGGCA 1980  
 QY 661 CysProValValProLeuTyrMetArgAspLysThrLeuIleGlnGluGlnTyrProLysAsp 680  
 DB 1981 TGCTCTGTGCTCTCTATGAGTGGGATAGACCTCTCACTTGAAGACAGTGGGAAAT 2040  
 QY 681 PheCysSerMetLeuGluYThrHisProHisLeuArgGlnLeuAspLeuGluYSerSerIle 700  
 DB 2041 TTCTGCTCATGCTTGGCACCCACCACTGGGGAGCTGAGCTGGGAGCAGCATC 2100  
 QY 701 LeuThrGluArgAlaMetLysThrLeuGlyAlaLysLeuArgHisProThrCysLysIle 720  
 DB 2101 CTGACAGAGCGGGCATGAGACCTGTGTGCCAAGCTGAGGCAATCCACCTGCMAAGATA 2160  
 QY 721 GlnThrLeuMetPheArgAsnAlaGlnIleThrProGluValGlnHisLeuTyrArgIle 740  
 DB 2161 CAGACCTGATGTTAGAAATGACACAGATACCTCTGTGTGCCAGACCTCTGGAGAAATC 2220  
 QY 741 ValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGluYThrHisLeuLysGlnGlu 760  
 DB 2221 GTCATGGCCAACTGAACTTAAGATCCTCAACTGGGAGGCACTGAGAGCAAG 2280  
 QY 761 AspValArgMetAlaCysGlnAlaLeuLysHisProLysCysLeuLeuGluSerLeuArg 780  
 DB 2281 GATGTAAGATGGCGCTGGAAGCCTTAAACACCCMAAATGTTGTGTGAGCTTGTAGG 2340  
 QY 781 LeuAspCysCysGluYLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeuThrThr 800  
 DB 2341 CTGATTCCTGTGATTAACCATGCTGTGTACTGAAAGATCTCCCAATCTTTCAGAC 2400  
 QY 801 SerProSerLeuLysSerLeuSerLeuAlaGluYAsnLysValThrAspGlnGluValMet 820  
 DB 2401 TCCCCAGACCTGAATCTCTGAGCTGGCAGGAAACAAAGTGACAGACAGGAGTAAATG 2460  
 QY 821 ProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAsp 840  
 DB 2461 CCTCTCAGTGAAGCTTGAAGAGTCTCCAGTGCCTGCGAGAACCTGATACCTGAGAGAC 2520  
 QY 841 CysGluYIleThrAlaThrGluYCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSer 860  
 DB 2521 TGTGGCAATCACAGCCAGCGGTGGCCAGAGTCTGCGCTCAAGCCCTGTCCAGAACCGGAGC 2580  
 QY 861 LeuThrHisLeuCysLeuSerAsnAsnSerLeuGluYAsnGluGluValAsnLeuLeuCys 880  
 DB 2581 TTGACACACCTGTGCTATCCAAACAGACCTGGGGAACGAAGGTAAATTAATCTATGTGT 2640  
 QY 881 ArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeu 900  
 DB 2641 CGATCCAGAGGCTTCCCACTGTAGTCTGACAGAGGCTGATGCTAACTCAAGCTGACACCTG 2700  
 QY 901 AspThrAlaGluYCysGluYPheLeuAlaLeuAlaLeuMetGluYAsnSerTyrLeuThrHis 920  
 DB 2701 GACACGGCTGGCTGTGGTTTCTTGCATCTGCGCTTAAGGTAACTCAAGCTGACACGAC 2760  
 QY 921 LeuSerLeuSerMetAsnProValGluAspAsnGluYValLysLeuLeuCysGluValMet 940  
 DB 2761 CTGACCTTATAGATGAACCTCTGTGAAGACATGGGTGAACCTCTGTGGCAGAGGTATG 2820  
 QY 941 ArgGluProSerCysHisLeuGlnAlaLeuGluGluLeuValLysCysHisLeuThrAlaAla 960  
 DB 2821 AGAGAACCATCTTGTATCTCTCAAGGACCTGGAGTTGTAAAGTGTATCTCAACCGCGCG 2880

QY 961 CysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeuAspLeu 980  
 DB 2881 TGCTGTGAGAGTCTGTCTGTGTATCTCGAGGAGACACCTGGAAGAGCTGATTC 2940  
 QY 981 ThrAspAsnAlaLeuGluYAspGluYValAlaAlaLeuCysGlnGluYLeuLysGlnLys 1000  
 DB 2941 ACGACAAATGCGGTGGAGCGGTGGGTGTCTGCTGCTGCAGAGGACTAAGCAAAAG 3000  
 QY 1001 AsnSerValLeuThrArgLeuGluYLeuLysAlaCysGluYLeuThrSerAspCysCysGlu 1020  
 DB 3001 AACAGTGTTCAGAGAGACTGGGTTGAAGCAATGGACATGACTGATTCATTCCTGTAG 3060  
 QY 1021 AlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsn 1040  
 DB 3061 GCACCTCTCTGGCCCTTCTCTGCAACCGGCAATCTGACCAAGCTCAAACTGTGTGAGAT 3120  
 QY 1041 AsnPheSerProLysGluYMetMetLysLeuCysSerAlaPheAlaCysProThrSerAsn 1060  
 DB 3121 AACTTCAGTCCCAAGAGATGATGAAGCTGTGTGCGCTTGGCTGTCCACGCTTAC 3180  
 QY 1061 LeuGlnIleIleGluYLeuTyrLysTyrProValGlnIleArgLysLeuLeuGlu 1080  
 DB 3181 TTACAGATTAATGGGCTGTGAATGGCAATGCACTGTGCAAAATAGAGAGCTGTGAG 3240  
 QY 1081 GluValGlnLeuLeuLysProArgValValIleAspGluYSerTyrPheAspGlu 1100  
 DB 3241 GAAGTGACGTAATCAAGCCCGAGTGTATTAATGAGTGTGATTCCTTGTATGAA 3300  
 QY 1101 AspAspArgHisLysIleGluYLeuThrPheArgLeuProGluYSerArgAlaTyrProCys 1120  
 DB 3301 GATGACCAACAAMATGAGACTTACTTCCGCTCCCTGAAGCGGGCAATGGCAGATG 3360  
 QY 1121 AlaLeuLeuTyrGluYMetAsnProGluGlnLysLysArgValSerLeuLeuAlaGluYAsp 1140  
 DB 3361 GCTTGTCTGTGGGATGAACCCAGAGCAAGAAAGCTGTGTCTCTCTGCTGAGAAC 3420  
 QY 1141 PheLysSerSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGluYGluSer 1160  
 DB 3421 TTCAAGACAGATGACAGATTTGCCAAGTCTCTGCTGCGCAACCGCAAAATGTGTAGTCC 3480  
 QY 1161 GlnArgValAspAsnValGluGlnSerSerProGlnProMetAlaGluYThrGlnHisLys 1180  
 DB 3481 CAGAGATTTGACCAAGTGGACAGAGCTCCCGCAACCAATGAGCGGACGGAACACAA 3540  
 QY 1181 GlnAspLysMetLeuSerValGluYTyrSerGluYAlaTyrSerGluThrAlaGluYLeuGlu 1200  
 DB 3541 CAAGATTAATGTTGAGTGTGATATTCGGAAGCTGTGTGAATCTGAGCTCGAA 3600  
 QY 1201 GlnLeuGluYSerAsnSerAlaAspHisAspHisGluYMetAlaTyrSerLeuGluYArg 1220  
 DB 3601 GGGCTTGATCAACAGTGCATGATCATGACCAAGGAGTATGGCTGTCACTAGGAGAG 3660  
 QY 1221 GlnLeuSerSerArgGluYLeuCysProThrValLeuMetThrThrAlaValCysProGlu 1240  
 DB 3661 GAGCTGAGCTGAGGGGCTGTGTGTCCAAAGTCTGATGACCAAGCGGTGTGCTGTGT 3720  
 QY 1241 HisTyrGluYArgLeuGluYSerArgGluYThrCysLeuAsnSerAlaAspAspHisSerGlu 1260  
 DB 3721 CACTGGAGCGGCTGGGCTCTAGGGGCTGTGTCTTAAAGTGTGATGACCAAGCGGCT 3780  
 QY 1261 ValSerTyrSerLeuGluYAlaAlaGluYLeuGluYLeuValSerAsnSerAlaAspAsp 1280  
 DB 3781 GTGTCTGTGTCACTGGAGCGGCTGGGCTCGAGGGGCTTGTGTCAACAGTGTCTATGAC 3840  
 QY 1281 HisSerGluYValAlaTyrSerLeuGluYAlaAlaGluYLeuGluYLeuValSerAsnSer 1300  
 DB 3841 CACAGCGGTGTGGCTGTGTCACTGGAGCGGCTGGGCTCGAGGGGCTTGTGTCAACAGT 3900  
 QY 1301 AlaAspAspHisSerGluYValSerTyrSerLeuGluYAlaAlaGluYLeuGluYLeuVal 1320  
 DB 3901 GCTGATGACCAAGCGGTGTGTCTGTGTCACTGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960  
 QY 1321 SerAsnSerAlaAspAspHisSerGluYValSerTyrSerLeuGluYAlaAlaGluYLeuGlu 1340

Db 3961 TCACAGAGTCTGATGACCAAGGGGTGTCTGCTGACCTGGAGGGGCTGGAG 4020  
QY 1341 GYLeuValSer 1344  
Db 4021 GGGCTGGTGTCT 4032

RESULT 3  
US-10-416-642-3  
; Sequence 3, Application US/10416642  
; Publication No. US20040043452A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: RAMKUMAR, JayaIaxmi  
; APPLICANT: ARVIZU, Chandra  
; TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS  
; FILE REFERENCE: PF-0842.PCT  
; CURRENT APPLICATION NUMBER: US/10/416,642  
; CURRENT FILING DATE: 2003-05-13  
; PRIOR APPLICATION NUMBER: 60/249,407  
; PRIOR FILING DATE: 2000-11-15  
; NUMBER OF SEQ. ID NOS: 4  
; SOFTWARE: PERL Program  
; SEQ. ID NO. 3  
; LENGTH: 3489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1  
US-10-416-642-3

Alignment Scores:  
Pred. No.: 0 Length: 3489  
Score: 5756.00 Matches: 1102  
Percent Similarity: 95.34% Conservative: 2  
Best Local Similarity: 95.16% Mismatches: 0  
Query Match: 81.37% Indels: 54  
Gaps: 1

US-10-066-521-6 (1-1344) x US-10-416-642-3 (1-3489)

QY 1 MetGluGlyAspIysSerLeuThrPheSerSerTyrlGlyLeuGlnTrpCysLeuTyrglu 20  
Db 1 ATGGAAGAGACAAATGCTCACCTTTTCAGCTACGGGCTGGCAATGCTGTCTATGAG 60  
QY 21 LeuAspIysGluGlnPheGlnThrPheIysGluLeuLeuIysIysSerSerGluSer 40  
Db 61 CTAGACAAAGAGAAATTTGAGACATTCAGAGAAATTTACTTAAAGAAATCTTCAGAAATCG 120  
QY 41 ThrThrCysSerIleProGlnPheGluIleGluAsnIleAsnValGluCysLeuAlaLeu 60  
Db 121 ACCACATGCTCTATTCACAGTTTGAATTCAGAAATCCAAAGTGAATGCTGGCACTC 180  
QY 61 LeuLeuHisGluTyrlGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80  
Db 181 CTCTGGATAGATTAATGAGATGCTGCTGGCTGGCTAGCTCACTTAGATCTTTGAA 240  
QY 81 AsnMetAsnLeuAlaGlnTrpLeuSerGluIysAlaArgAspAspMetCys----- 96  
Db 241 AACATGAACCTGGCAACCTCTCGAGAAAGGCAAGGATGACATGAATAATTCACAGAA 300  
QY 96 ----- 96  
Db 301 GATTCCTAGACACAGATGACTGACCAAGACCAAGCAAGAAAAAGTCCAGAAAAATMAA 360  
QY 96 ----- 96  
Db 361 TATGACATGACTAAGCTTATCTGGGGGTGTGACATCTCTGACCTGCAATTAATAACAC 420  
QY 97 -----LysIleSerGlnAlaMetGluGlnGluGly 106  
Db 421 AAGTATGTGAATTCATCTTCTTTTGCAGAAATTCACAAAGCTATGGAACAGAAAGGT 480

QY 107 AlaThrAlaIleGluThrGluGlnGluGlnIleSerGlnAlaMetGluGlnGluGlyAla 126  
Db 481 GCCACAGCAGCAGACAGACAGAAAGAAATTTCCAGACTATGGAACAGAAAGGTGCC 540  
QY 127 ThrAlaIleGluThrGluGlnGluGlnIleGlyIleGlyIleAspThrTrpAspTyrlYsSerHis 146  
Db 541 ACAGCAGCAGACAGACAGAAAGCAAGACATGGAGGTGACATAGGCACTACAGAGCTCAC 600  
QY 147 ValMetThrIysPheAlaGluGlnGluGlnIleAspValArgSerPheGluAsnThrAlaAla 166  
Db 601 GTATGACCAATTCGCTGAGAGAGATGTACGTCTGATTTGAAAAACATGCTGCT 660  
QY 167 AspTrpProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTrpGlyPheArg 186  
Db 661 GACTGGCCGGAATGCAACGTTGGCTGGTCTTTGATTCAACAGCGGTGGCTTCGG 720  
QY 187 ProArgThrValIleLeuHisGlyIysSerGlyIleGlyIysSerAlaLeuAlaArgArg 206  
Db 721 CTTCGACAGGTGGTCTGACAGGAAAGTCAGAAATTTGGAAATCGGCTCTAGCCAGAAAG 780  
QY 207 IleValLeuCysThrAlaGlnGluGlyLeuTyrlGlnGlyMetPheSerTyrlValPhePhe 226  
Db 781 ATGGTGTGTGTGGGGGCAAGGTGACCTTACAGGAAATGTCTCTTCGTCTTCTTC 840  
QY 227 LeuProValArgGluMetGlnArgIysGlyGluSerSerValThrGluPheIleSerArg 246  
Db 841 CTCCTCCGTTAGACAGATGACGCGAAGAGAGAGAGCTGTCAACAGTTTCATCTCAGG 900  
QY 247 GluTrpProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeuLeu 266  
Db 901 GAGTGGCACAACCTCCAGGCTCCGGTGAACGAGATCATGTCCGACACAGAAAGCTGTTG 960  
QY 267 PheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrIysLeuCys 286  
Db 961 TTCACTCATTCACGTTTCATGATGACTGGGCTCTGTCTCAACAATGACAAAGCTCTGC 1020  
QY 287 LysAspTrpAlaGluIysGlnProProPheThrLeuIleArgSerLeuLeuArgIysVal 306  
Db 1021 AAAGACTGGGCTGAGAAAGCAGCTCCGTTCACTCATAGCAGTGTGAGAGAAAGTTC 1080  
QY 307 LeuLeuProGluSerPheLeuIleValThrValArgAspValGluThrGluIysLeuIys 326  
Db 1081 CTGCTCCCTGAGTCTCTTCATGATGCTGATGCTGACCGTGAAGACCTGGGCAACAGAAAGCTCAG 1140  
QY 327 SerGluValIleSerProArgTyrlLeuLeuValArgGlyIleSerGlyGluGlnArgIle 346  
Db 1141 TCAAGGTGTGTCTCCCTCCGTACCTGTGTTAGAGAAATCTCCGGGAAACAAGAAATC 1200  
QY 347 HisLeuLeuLeuGluArgGlyIleGlyGluHisGlnIysThrGlnGlyLeuArgAlaIle 366  
Db 1201 CACTGTCTCTTAGCGCGGGGATTTGGTGAACATCAAGAAACAGAGGTTGCGTGCATC 1260  
QY 367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCys 386  
Db 1261 ATGAACAACCGTAGCTGCTGACCAAGTGCAGAGTGCCTCCGCTGCTCTCATCTGC 1320  
QY 387 ValAlaLeuGlnLeuGlnAspValIleGlyGluSerValIleProPheAsnGlnThrLeu 406  
Db 1321 GTGGCTCTGAGCTGACGAGCGTGTGGGGAAGAGCTCCCTCCCTTCAACCAAGCTTC 1380  
QY 407 ThrGlyLeuHisAlaIlePheValPheHisGlnLeuThrProArgGlyValIleArgArg 426  
Db 1381 ACAAGCTGACCGCGCTTTTGTGTTTCATCACTCAACCTCCGAGCGGTGCTCCGGCGC 1440  
QY 427 CysLeuAsnLeuGluGluArgValIleLeuIysArgPheCysArgMetAlaValGluGly 446  
Db 1441 TGTCTCAATCTGAGGAAAGATTTGCTGAAACGCTTCTGCGGTATGGGTGGAGGGA 1500  
QY 447 ValTrpAsnArgIysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGlu 466  
Db 1501 GTGTGAATGAGAAATCATGTGTTTGAACGTGACGACCTCATGTTCAGAACTCGGGAG 1560

QY 467 SerGluLeuArgAlaLeuPheH1eMeCAsn1LeuLeuProAspSerH1eCyGlu1u 486  
 DB 1561 TCTAGCTCCGCTGCTGTTTCACTGAATCTCTTCTCCAGACAGCACTGAGAG 1620  
 QY 487 TTTTThrPhePheH1eLeuSerLeuGlnaPheCyAla1aLeuTyrTyrValLeu 506  
 DB 1621 TACTACACCTTCTTCCACTCAGTCTCCAGAGCTTGTGTGCGCTTACTACAGTGTTA 1680  
 QY 507 GluGluLeuGlu1LeuProAlaLeuCyProLeuTyrValGluValThrLeuArgSer 526  
 DB 1681 GAGGCGCTGGAATCGAGCCAGCTCTCTGCGCTGTGAGTGAAGAACAAAGAGTCC 1740  
 QY 527 MetGluLeuArgAlaGlyPheH1e1LeuSerLeuTyrMetLeuArgPheLeuPhe 546  
 DB 1741 ATGAGAGCTTAAACAGGAGGCTTCCATCCACTGCTTGTGAGTGAAGCGTTTCTGTTT 1800  
 QY 547 GlyLeuValSerGluAspValaArgArgProLeuGluValLeuLeuGlyCyProValPro 566  
 DB 1801 GGCTCTGAGAGCAAGAGTGAAGAGGCACTGAGAGTCTGTGCGCTGTCCGCTTCC 1860  
 QY 567 LeuGlyValIlyGlnIlyLeuLeuH1eTyrValSerLeuLeuGlyGlnIlyProAsnAla 586  
 DB 1861 CTGGGGGTGAAGCAGAACCTTCTGCACTGGGTCTCTGTGGTGAAGCAGCTTATATCC 1920  
 QY 587 ThrThrProGlyAspThrLeuAspAlaPheH1eCyLeuPheGluThrGlnaAspIlyGlu 606  
 DB 1921 ACCACCCAGAGAGACCCCTGAGCCCTTCCACTCTTCTTTCGACATCCAGAACAAAG 1980  
 QY 607 PheValaArgLeuAlaLeuAsnSerPheGlnGluValaTyrLeuProIleAsnGlnaAsnLeu 626  
 DB 1981 TTTGTGCTTGGCTTGAATTAACAGCTTCCAGAAAGTGGCTTCCGATTAAACAGAACTCG 2040  
 QY 627 AspLeuIleAlaSerSerPheCyLeuGlnH1eCyProTyrLeuArgIlyLeuArgVal 646  
 DB 2041 GACTGATAGACATCTTCTCTGCTCCAGCAGCTCTCCGATTTTCGGAATAATTCGGGTG 2100  
 QY 647 AspValIlyGlyIlePheProArgAspGluSerAlaGluAlaCyProValaIlyProLeu 666  
 DB 2101 GATGCAAAAGGATTTCCCAAGAGATGATCGCTGAGGAGCATGCTGTGCTCTCTTA 2160  
 QY 667 TrpMetArgAspIlyThrLeuIleGluGluGlnTyrGluAspPheCySerMetLeuGly 686  
 DB 2161 TGGAGCGCGGATTAACCTCTCATTAAGAGAGAGTGGAAAGATTTCGTCCATGCTTGGC 2220  
 QY 687 ThrH1eProH1eLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMet 706  
 DB 2221 ACCCACCAACACTCGGAGAGCTGAGCCTGGGAGCAGCATCTGACAGAGGGGCCATG 2280  
 QY 707 LysThrLeuCyValaIlyLeuArgH1eProThrCyIlyValIleGlnThrLeuMetPheArg 726  
 DB 2281 AAGACCTGTGTGCAAGCTGAGGCACTCCACTGACATACAGAACCTGTAGTTTAA 2340  
 QY 727 AsnAlaGlnIleThrProGlyValaGlnIleLeuTyrArgIleValaMetAlaAsnArgAsn 746  
 DB 2341 AATGACACAGATTACCTCGTGTGTGAGCAGCCTCTGGAAGATGTCATGCGCAACCTGTA 2400  
 QY 747 LeuArgSerLeuAsnLeuGlyIlyThrH1eLeuGlyGluGluAspValaArgMetAlaCy 766  
 DB 2401 CTAAATGCTCTCAACTGGAGGAGCACTCCAGAAAGAAAGATGTAAGATGCGTGT 2460  
 QY 767 GluAlaLeuIlyPheIlyProIlyCyLeuLeuGluIlySerLeuArgLeuAspCyCyGlyLeu 786  
 DB 2461 GAAGCTTAAACACCCCAAAAGTTGTGTGAGTCTTGAAGCTGATGCTGTGATTTG 2520  
 QY 787 ThrH1eAlaCyTyrLeuIlyIleSerGlnIleLeuThrThrSerProSerLeuIlySer 806  
 DB 2521 ACCCATGCTGTACTGTAAGATCTCCAAATCTTTAGACACTCCCGCCAGCTGAATAT 2580  
 QY 807 LeuSerLeuAlaGlyAsnIlyValaThrAspGlnGlyValaMetCyProLeuSerAspAlaLeu 826  
 DB 2581 CTGACCTGTGAGAAACAAAGGTGACAGACAGGAGTATATGCTCTCAGTATGCTTGG 2640  
 QY 827 ArgValSerGlnCyAlaLeuGlnIlyLeuIleLeuGluAspCyGlyIleThrAlaThr 846

DB 2641 AGAGTCTCCAGTCCGCTTGCAGAACTGATTAAGAGAGCTGTGGATCAACAGCCAG 2700  
 QY 847 GlyCyGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrH1eLeuCyLeu 866  
 DB 2701 GGTTGCAAGTCTGGCTTCCAGCTTGTGAGCAACCGAGACTTGAACACTGTGCTTA 2760  
 QY 867 SerAsnSerLeuGlyAsnGluIlyValaAsnLeuCyAspSerMetArgLeuPro 886  
 DB 2761 TCCAAACACCTCGGGAGAGAGTGTAAATTAATCACTGTGTCAATCAATAGGCTTCC 2820  
 QY 887 HisCySerLeuGlnaArgLeuMetLeuAsnGlnCyH1eLeuAspThrAlaGlyCyGly 906  
 DB 2821 CACTGATGTGAGAGGCTGATGCTGAATCAGTCCACTGAGCAGCGCTGGCTGTGT 2880  
 QY 907 PheLeuAlaLeuAlaLeuMetGlyAsnSerThrLeuThrH1eLeuSerLeuSerMetAsn 926  
 DB 2881 TTTCTTGCACTTGGCTTATGGTAACTCAATGCTGAGCAGCCTGAGCTTAAGCATGAA 2940  
 QY 927 ProValaGluAspAsnGlyValaIlyLeuLeuCyGluValaMetArgGluProSerCyH1e 946  
 DB 2941 CTTGTGAAGCATGTGGCTGAACCTTGTGCGAGTCAATGAGAACCATCTTGTCTAT 3000  
 QY 947 LeuGlnaPheLeuGluLeuValaIlyCyH1eLeuThrAlaAlaCyCyGluSerLeuSer 966  
 DB 3001 CTCAGAGACTGAGTGTGTAAGTGCATCTCAACCGCGGTGCTGAGAGTCTGTCC 3060  
 QY 967 CyValaIleSerArgSerArgH1eLeuIlySerLeuAspLeuThrAspAsnAlaLeuGly 986  
 DB 3061 TGTGTGATCTGAGAGAGAGACACTGAAGAGCTGAGATTCACAGACAAATGCTTGAGT 3120  
 QY 987 AspGlyValaIleAlaLeuCyGluIlyLeuIlyGlnIlyAsnSerValLeuThrArg 1006  
 DB 3121 GAGGTGGGTGCTGCTGCACTGTGCGAGGAGCTGAAGCAAAAGAACAGTTCGAGGA 3180  
 QY 1007 LeuGlyLeuIlyAlaCyGlyIlyLeuThrSerAspCyGluAlaLeuSerLeuAlaLeu 1026  
 DB 3181 CTGGGTGAAGGATGAGCTGACTGACTTGTGCTGTGAGGCACTCTCTGCGCCCTT 3240  
 QY 1027 SerCyAsnArgH1eLeuThrSerLeuAsnLeuValaGlnaAsnPheSerProIlyGly 1046  
 DB 3241 TCTTGCAACCGGCACTGACCAAGCTTAACTGTGCGAAATTAATTAAGTCCCAAGAA 3300  
 QY 1047 MetMetIlyLeuCySerAlaPheAlaCyProThrSerAsnLeuGlnIleGlyLeu 1066  
 DB 3301 ATGATGAAGCTGTGTGCTGCGCTTGTGCTGTCCAGCTTAATTAAGATTAATGGCGT 3360  
 QY 1067 TrpLysTyrGlnTyrProValaGlnIleArgIlyLeuLeuGluGluValaGlnLeuLeuIly 1086  
 DB 3361 TGGAAATGGAGTACCTGTGCAATTAAGAGAGTGTGAGAGAGTCAAGTCAAGTCAAG 3420  
 QY 1087 ProArgValaIleAspGlySerThrPheIlySerPheAspGluAspArgH1e 1104  
 DB 3421 CCCCGAGTGTAAATGACGTGATGTCATCTTGTATGAAGATGACCGGTAC 3474

RESULT 4  
 US-10-216-645-1  
 ; Sequence 1, Application US/10216645  
 ; Publication No. US20030125282A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEISS, BERTRAM  
 ; APPLICANT: LESSL, MONIKA  
 ; APPLICANT: PETERS-KOTTIG, MICHAEL  
 ; APPLICANT: BECKMANN, GEORG  
 ; TITLE OF INVENTION: HUMAN MATER PROTEINS  
 ; FILE REFERENCE: SCH-1910  
 ; CURRENT APPLICATION NUMBER: US/10/216,645  
 ; CURRENT FILING DATE: 2003-01-21  
 ; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41  
 ; PRIOR FILING DATE: 2001-08-10  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1

LENGTH: 3926  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-216-645-1

## Alignment Scores:

Pred. No.:	0	Length:	3926
Score:	5756.00	Matches:	1102
Percent Similarity:	95.34%	Conservative:	2
Best Local Similarity:	95.16%	Mismatches:	0
Query Match:	81.37%	Indels:	54
DB:	6	Gaps:	1

US-10-066-521-6 (1-1344) x US-10-216-645-1 (1-3926)

QY 1 MetGluGlyAspLysSerLeuThrPheSerSerTyrGlyLeuGlnTyrCysLeuTyrGlu 20  
DB 1 ATGGAAGGACAAATGCTCACCTTTTCCAGCTACGGCTGCATGCTGTCTCTATGAG 60  
QY 21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLeuLysLysLysSerSerGluSer 40  
DB 61 CTGACACAGAAAGATTTCAGACATTCAAGGAATTACTAAAGAAATCTTCAGATCG 120  
QY 41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60  
DB 121 ACCACATGCTCTATTCCACAGTTTGAATCGAAGATCCAAACGTGGAATGCTGGCACATC 180  
QY 61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaThrAlaThrSerIleSerIlePheGlu 80  
DB 181 CTCTTGATAGATTATTAAGACATCGCTGGCTGGCTAGCTCATTCATTCATCTTTGAA 240  
QY 81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspAspMetLys----- 96  
DB 241 AACTGACCTCGGACCCCTCTCGGAGAGGACGCGGATGACATGAAGAAATTCACAGAA 300  
QY 96 ----- 96  
DB 301 GATCCTGAACCAAGATGATGACCAAGACCAAGAAAGAAAGTCCAGAAATATAA 360  
QY 96 ----- 96  
DB 361 TATGGCATGACTAAGCTTATCTGGGGGTCTGACATCTCTGACTCGAATATATAAC 420  
QY 97 -----LysIleSerGlnAlaMetGluGlnGlu 106  
DB 421 AAGTATGTGAATTCATCTCTTTTTCAGAAATTTCAACAGCTTAGGAACAAAGGT 480  
QY 107 AlaThrAlaAlaGluThrGluGluGluIleSerGlnAlaMetGluGlnGluVal 126  
DB 481 GCCACACAGACAGACAGAAAGAAACAAGAAATTCACAGCTATGGAACAAAGGTGCC 540  
QY 127 ThrAlaAlaGluThrGluGluGluIleHisGlyValAspThrThrPhePheSerHis 146  
DB 541 ACAGACACAGACAGAAAGAAACAAGACATGAGGTGACACATGGACTACAGAGTAC 600  
QY 147 ValMetThrLysPheAlaGluGluGluLysAspValArgArgSerPheGluAsnThrAla 166  
DB 601 GTGATGACCAATTCGCTGAGGAGAGAGATGTAAGTGTAGTTTGAACAACATGCTGCT 660  
QY 167 AspTyrProGluMetGlnThrLeuAlaGlyAlaPheAspSerAspArgTyrGlyPheArg 186  
DB 661 GACTGCGCGGAAATGCAAAAGCTTGCTGCTGCTTTTATTCAGACCGGTGGGCTCCGG 720  
QY 187 ProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArg 206  
DB 721 CTCTGCACGGGTGCTTGCACGGAAAGTCAGAAATGGGAAATGGCTTAGCCAGAGG 780  
QY 207 IleValLeuCysTyrAlaGlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePhe 226  
DB 781 ATCGTGTGCTGCTGGGCGAAAGTGAAGTCTACCAAGGAATGTTCTCTAGCTTTCTTC 840  
QY 227 LeuProValArgGluMetGlnArgLysLysGluSerSerValThrGluPheIleSerArg 246

DB 841 CTCCTCCGTTAGAGATGACGCGAAGAGAGAGACAGTGTCAAGAGTTTCATCTCCAGG 900  
QY 247 GluTyrProAspSerGlnAlaProValThrGluIleMetSerArgProGluArgLeuLeu 266  
DB 901 GAGTGGCCAGACTCCAGAGCTCCGGTGAAGGAATCATGTCTCCGACCAAGAAAGGCTGTG 960  
QY 267 PheIleLeuAspGlyPheAspAspLeuGlySerValLeuAsnAsnAspThrLysLeuCys 286  
DB 961 TTCATCATTAACGGTTTCATGATGACCTGGGCTGTCTCTCAACAATGACACAAAGCTTGC 1020  
QY 287 LysAspTyrAlaGluLysGlnProProPheThrLeuIleArgSerLeuLeuArgVal 306  
DB 1021 AAGACTGGGCTAGAAAGAGCTCCGTTACCTCATACAGTGTGTGAGGAGAGTTC 1080  
QY 307 LeuLeuProGluSerPheLeuIleValThrValArgAspValGlyThrGluLysLeuLys 326  
DB 1081 CTGCTCCCTTAGTCTCTTCGATCTGACCGTTCAGAGACCTGGGGCACAGAAAGCTCAAG 1140  
QY 327 SerGluValValSerProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIle 346  
DB 1141 TCAGAGGTGCTGTCTCCCGTACCTGTAGTGAAGAAATCTCCGGGGAAACAAAGATC 1200  
QY 347 HisLeuLeuLeuGluArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIle 366  
DB 1201 CACTGTCTCTTAGAGCGGGATTTGGAGCATCAAGACACAGAGGTTGCTGCATC 1260  
QY 367 MetAsnAsnArgGluLeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCys 386  
DB 1261 ATGAACACACGTAAGCTCTGCACACAGTGCAGGTGCCCGGTGGCTCTCATATGTC 1320  
QY 387 ValAlaLeuGlnLeuGlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeu 406  
DB 1321 GTGGCCCTGACGTGACGACGCTGGGGGAAAGACCTCCCTTCAACCAACCTC 1380  
QY 407 ThrGlyLeuHisAlaAlaPheValPheHisGlyLeuThrProArgValValArgArg 426  
DB 1381 ACAGGCTTGACCGCTTTTGTTCATCACTGACCTCCCTGAGCGGTGGTCCGGC 1440  
QY 427 CysLeuAsnLeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGly 446  
DB 1441 TGTCTCAATCTGAGAGAAAGATTTCTCTGAAGCGCTTGCCTGATGGCTGGAGAGGA 1500  
QY 447 ValTyrAsnArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGly 466  
DB 1501 GTGGGAATGGAAGTACAGTGTGACGTGACGACCTCATGTGTTCAAGACCTCGGGAG 1560  
QY 467 SerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCysGluGlu 486  
DB 1561 TCTGAGCTCGGTCTGTGTTCAATGACATGCACTCTTCCAGACGCCACTGTAGAGAG 1620  
QY 487 TyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrValLeu 506  
DB 1621 TACTACACCTTTCTTCCACTCACTCAGAGCTTGTGTCGGCTGTGTAAGTGTGTA 1680  
QY 507 GluGlyLeuGluIleGluProAlaLeuCysProLeuTyrValGlyLysThrLysSer 526  
DB 1681 GAGGGCTGGAATCGAGCAGCTCTGCTCTGTACCTTGAGAAAGAAAGAGTTC 1740  
QY 527 MetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuThrPheLysArgPheLeuPhe 546  
DB 1741 ATGGAAGTTTAAACAGGAGGCTTCATATGCACTCGCTTGGATGAAGCTTTCTTGT 1800  
QY 547 GlyLeuValSerGluAspValArgArgProLeuGluValLeuLeuGlyCysProValPro 566  
DB 1801 GGCTCTGAGCGAAGACGTAAGAGGCCACTGGAAGTCCGTGCGGTGCTGCCGTTCCC 1860  
QY 567 LeuGlyValLysGluLysLeuLeuHisTyrValSerLeuLeuGlyGlnGlnProAsnAla 586  
DB 1861 CTGGGGGTGAAGCAGAAAGTTCGCACTGGGTCTCTGTGGGTCAAGACCTTAAAGCC 1920  
QY 587 ThrThrProGluAspThrLeuAspAlaPheHisCysLeuPheGlnThrGlnAspLysGlu 606  
DB 1921 ACCACCCAGAGACACCTGAGCGCTTCCACTGTCTTTTCCAGACTCAAGACAAAGAG 1980

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QY 607 PheValAlaLeuAlaSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeu 626
Db 1981 TTGTTGGCTTGGATTAAACAGCTTCCAGAAAGTGGCTTCCGATTAAACAGAACCTG 2040
QY 627 AspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuArgLysIleArgVal 646
Db 2041 GACTGTAGATGATCTTCTCTGCTCCAGACAGCTGCGTATTTGGGAAATTCGGGGTGG 2100
QY 647 AspValIleGlyIlePheProArgAspGlnSerAlaGluAlaCysProValValProLeu 666
Db 2101 GATGTCAAGAGGATCTTCCCAAGAGATGATCCGCTGAGGATGCTGCTGCTCTCTTA 2160
QY 667 TrpMetArgAspLysTrpLeuIleGlnGluGlnTrpGluAspPheCysSerMetLeuGly 686
Db 2161 TGGATGGGGATTAAGACCTCTCATTTGAGAGCATGGGAAATTTCTGCTCCATGCTTGGC 2220
QY 687 ThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgLamMet 706
Db 2221 ACCCAACCAACACCTGGGCACTGGACCTGGGCAAGACATCTTGACAGACGGGCCATG 2280
QY 707 LysThrLeuCysAlaLysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArg 726
Db 2281 AAGACCTGTGTGCCAAGCTGAGGATCCCACTGCAGATACAGACCTGATGTTTGA 2340
QY 727 AsnAlaGlnIleThrProGlyValGlnHisLeuTrpArgLysIleMetAlaAsnArgAsn 746
Db 2341 AATGCACAGATTACCTCTGTGTGAGACACCTTGGAATATGCTATGGCCACCGTAAAC 2400
QY 747 LeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGlnGluAspValArgMetAlaCys 766
Db 2401 CTTAAGATCCCTCAACTTGGAGGACCCACCTGAAGAAAGAGATGAAGATGGCGGT 2460
QY 767 GluAlaLeuLysHisProLysCysLeuLeuGlnSerLeuAlaGluAspCysGlyLeu 786
Db 2461 GAAGCTTAAACACCCCAAAATGTTTGTGAGTCTTGAAGCTGATGCTGTGGATTG 2520
QY 787 ThrHisAlaCysTyrTrpLeuLysIleSerGlnIleLeuThrTrpSerProSerLeuLysSer 806
Db 2521 ACCCAATGCTGTATCTTAAGATCTCCCAATCTTACAGACCTCCCAAGCTGAAATCT 2580
QY 807 LeuSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeu 826
Db 2581 CTGAGCCTGGCAGAGAAACAAGTGAACAACAGGAGATGAAGCTCTCAAGATGCCCTTG 2640
QY 827 ArgValSerGlnCysAlaLeuGlnLysLeuIleLeuGluAspCysGlyIleThrAlaThr 846
Db 2641 AAGATCTCCAGATGCGCCTGCAAGAGCTGATACCTGAGAGACTGTGGCATCACACCG 2700
QY 847 GlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeu 866
Db 2701 GGTGGCCAGAGTCTGGCTCAGCCCTCTGTCAAGCAACCGAGCTTACACACCTGTGCTTA 2760
QY 867 SerAsnAsnSerLeuGlyAsnGlnGlyValAsnLeuLeuCysArgSerMetArgLeuPro 886
Db 2761 TCCAAACAACAGCTGGGGAACAAGGTAAATCTACTGTGTGATTCATAGAGCTTCCC 2820
QY 887 HisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGly 906
Db 2821 CACTGTAGCTGCAAGAGCTGATGCTGAATCAGTCCACCTGACACAGCGCTGGCTGTGT 2880
QY 907 PheLeuAlaLeuAlaLeuMetClyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsn 926
Db 2881 TTTCTTGACCTGCTTATGGGTAACTCATGTGTCAGCACCTTAAGCCTTAAGCATGAAC 2940
QY 927 ProValGluAspAsnGlyValLysLeuLeuCysGluValMetArgLysProSerCysHis 946
Db 2941 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCAATAGAGAACCATCTTGAT 3000
QY 947 LeuGlnAspLeuGlnLeuValLysCysHisLeuThrAlaAlaCysCysGlnSerLeuSer 966
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QY 967 CysValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGly 986
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QY 987 AspGlyGlyValAlaAlaLeuCysGlnGlyLeuLysGlnLysAsnSerValLeuThrArg 1006
Db 3121 GACGATGGGCTTGTGACCTGTGCAAGAGGAGTGAAGCAAAAGAACAGGTCTGACAGGA 3180
QY 1007 LeuGlyLeuLysAlaCysGlyLeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeu 1026
Db 3181 CTCGGGTGAAGGAGATGTGACCTGATCTGATGCTGTGAGGACATCTCTTGGCCCTT 3240
QY 1027 SerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLysGly 1046
Db 3241 TCTGCAACCGGACATGACCAAGCTTAACCTGGTGCAGATTAATCTTCAAGTCCAAAGGA 3300
QY 1047 MetLeuLysLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLeu 1066
Db 3301 ATGATGAAGCTGTGTGGCTTGGCTTGCCTCCACGCTTAACCTTACATATATTGGGCTG 3360
QY 1067 TrpLysTrpGlnIleProValGlnIleArgLysLeuGlnGluValGlnLeuLeuLys 1086
Db 3361 TGAATAAGGCAATCCCTGTGCATAATAGAAAGCTCTGGAGGAAGTGCAGTCACTCAAG 3420
QY 1087 ProArgValValIleAspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
Db 3421 CCCGAGTGTATTAATGAACGATGATGGATCTTTGATGAATGACCGGTAC 3474

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RESULT 5
US-10-860-761-3
; Sequence 3, Application US/10860761
; Publication No. US2004024875A1
; GENERAL INFORMATION:
; APPLICANT: WYETH
; TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
; FILE REFERENCE: AM101318
; CURRENT APPLICATION NUMBER: US/10/860, 761
; CURRENT FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3885
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3603)
US-10-860-761-3

Alignment Scores:
Pred. No.: 0 Length: 3885
Score: 5741.50 Matches: 1098
Percent Similarity: 96.16% Conservative: 3
Best Local Similarity: 95.90% Mismatches: 3
Query Match: 81.16% Indels: 41
DB: 8 Gaps: 1

US-10-066-521-6 (1-1344) x US-10-860-761-3 (1-3885)
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Db 154 ATGGAAGAGACAATATGCTCACTTTCACAGCTACGGGCTGCAATGCTGTCTATGAG 213
QY 21 LeuAspLysGlnGluPheGlnThrPheLysGlnLeuLeuLysLysLysSerSerGlnSer 40
Db 214 CTAGCAAGAGAAATTTCAACATTCACAGATTCACAGAAATTAAGAAATTTCAAGATTCG 273
QY 41 ThrThrCysSerIleProGlnPheGlnIleGlnAsnAlaAsnValGluCysLeuAlaLeu 60
Db 274 ACCAATCTCTATTCCACAGTTTGAATTCAGAAATCCAGAAATCCAGATGCTGGCACTC 333
QY 61 LeuLeuHisGlyTyrTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSerIlePheGln 80

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Dh 334 CTCCTGATGAGTATTATGAGGATCGCTGGCTGAGCTCATTCATCTTTGAA 393  
Qy 81 AAsMetAsnLeuArgThrPheLeuSerGluValAspAspMetLeuVal----- 97  
Dh 394 AACATGAACCTGCAACCTCTCTCGAAGAGGACAGGATGACATGAAGAATTCACCA 453  
Qy 97 ----- 97  
Dh 454 GAAGATCCTGAAGCAAGATGACTGACCAAGACCAAGCAAGAAAAAGTCCAGAAATT 513  
Qy 98 -----11Ser 99  
Dh 514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGACGAAAAAGAACGAATTTCA 573  
Qy 100 GlnAlaMetGluGlnGlnGluValaThrAlaAlaGluThrGluGlnGlnIleSerGln 119  
Dh 574 CAAGCTATGGAACAAGAAAGGTGCCACAGCAGACAGACAGAAAGAAATTTCAAA 633  
Qy 120 AlaMetGluGlnGluValaThrAlaAlaGluThrGluGlnGlnIleSerGluValAsp 139  
Dh 634 GCTATGGAACAAGAAAGGTGCCACAGCAGACAGACAGAAAGCAATGAGAGTGAC 693  
Qy 140 ThrTrpAspTyrIlePheSerHisValMetThrIlePheAlaGluGluValAspValArgArg 159  
Dh 694 ACATGGGACTACAAAGATGACGCTGATGACCAAAATTCCTGAGAGAGATGACCTGCT 753  
Qy 160 SerPheGluThrThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGluValaPheAsp 179  
Dh 754 AGTTTAAACACCTGCTGCTGACTGACGCGAAGATGCAAGCTTGCTGCTTTTGAT 813  
Qy 180 SerAspArgTrpGluPheArgProArgThrValaValaLeuHisGluIleValSerGluIleGly 199  
Dh 814 TCAGACCGGTGGGCTTCGGGCTTCGACGCGTGGTTCTGCACGGAAGTCAGAAATTGGG 873  
Qy 200 LysSerAlaLeuAlaArgGluIleValaLeuGluSerThrAlaGlnGluGluValaLeuGluGly 219  
Dh 874 AAATCGGCTCTAGCCAGAAAGATGCTGCTGCTGGCGCAAGGTGAGCTCTTACAGAGGA 933  
Qy 220 MetPheSerTyrValaPhePheLeuProValArgGluMetGlnArgGluValaLeuGluSer 239  
Dh 934 ATGTTCTCTTACGTTCTTCTCTCCGTTTGAAGATGACGCGGAAGAAAGAGAGAGT 993  
Qy 240 ValThrGluPheIleSerArgGluTrpProAspSerGlnAlaProValThrGluIleMet 259  
Dh 994 GTCAACAAGTTCACTCCAGGAGATGGCCAGACTCCAGGCTCGGTGACGAGATCATG 1053  
Qy 260 SerArgProGluArgLeuPheIleIleAspGluPheAspPheLeuGluSerValaLeu 279  
Dh 1054 TCCCGACCAAGAAAGCTGTTGTTCTCATTTGACGAGTTCATGACCTGGGCTCTGCTCTC 1113  
Qy 280 AsnAspAspThrIleValaLeuValaAspThrAlaGluValaGlnProPhePheThrLeuIle 299  
Dh 1114 AACATATACAAAGCTCTGCAAAAGCTGGCTGAAGAGAGAGCTCGGTTCACCTTCAATA 1173  
Qy 300 ArgSerLeuLeuArgValaLeuLeuProGluSerPheLeuIleValaThrValaArgAsp 319  
Dh 1174 CGCAGTCTGCTGAAGAAAGTCTGCTCCCTCGTGAAGCTTCCTGATCGTACACCTGAGAC 1233  
Qy 320 ValGluThrGluValaLeuValaSerProArgTyrLeuLeuValaArgGly 339  
Dh 1234 GTGGGCAAGAGAAAGCTCAAGTCAAGGTCGTGCTCCCTTACCTGTTAGTTAGAGGA 1293  
Qy 340 IleSerGluGluGlnArgGluIleIleLeuLeuGluGlnArgGluIleGluGluHisGluLys 359  
Dh 1294 ATCTCCGGGAAACAAGATCACTTGTCTTTAGAGCGCGGAGATTGGAGATCAAGAG 1353  
Qy 360 ThrGlnIleLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGlnCysGlnValaPro 379  
Dh 1354 ACAACAAGGTTGGCTGATCATCAACAACCGTAGGCTGCTGACCAAGTGCAGAGTGCC 1413  
Qy 380 AlaValaGluSerLeuIleCysValaAlaLeuGlnLeuGlnAspValaValaGluSerVala 399  
Dh 1414 GCCGTGGGCTCTCTCATCTGTGGTGGCTGTGACGCTGCAGACGTTGGGGGAGAGCGTCT 1473

Qy 400 AlaProPheAsnGlnThrIleuThrGluLeuHisAlaAlaPheValaPheHisGlnLeuThr 419  
Dh 1474 GCCCCTTCAACCAAAAGCTCACAGGCTGTGCAGCGCGCTTTTGCATTGATCAGCTACCC 1533  
Qy 420 ProArgGluValaValaArgArgCysLeuAsnLeuGlnGluArgValaValaLeuValaPhe 439  
Dh 1534 CCTCGAGGCTGTGCGCGCTGTCTCAATCTGGAGAAAGATTTGCTCGAAGCGCTTC 1593  
Qy 440 CysArgMetAlaValaGluGluValaTrpAsnArgLysSerValaPheAspGluAspAspLeu 459  
Dh 1594 TGCCTGATGCTGTGAAGGAGTGTGGAATGGAAGTCACTGTTTATGATGAGACCTTC 1653  
Qy 460 MetValaGlnIleuGluGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479  
Dh 1654 ATGTTTCAAGAGATCCGGGAGAGTGAAGCTCGGTCTGTGTTTCAATGAACATCTTCTC 1713  
Qy 480 ProAspSerHisCysGluGluTyrTyrThrPhePheHisIleuSerLeuGlnAspPheCys 499  
Dh 1714 CCAGACAGCCACTGTAGAGAGTACTACACTTCTCCACTCAGTCTCCAGAGCTTCTGT 1773  
Qy 500 AlaAlaLeuThrTyrThrValaLeuGluGluIleGluProAlaLeuCysProLeuTyr 519  
Dh 1774 GCCGCTGTGACTACGTTTGAAGGCTGGAATGAGACCACTCTTCCCTCTGTAC 1833  
Qy 520 ValGluIleThrIleAspSerMetGluLeuIleGlnAlaGluPheHisIleHisSerLeu 539  
Dh 1834 GTTGAGAAGCAAAAGAGTCCATGAGACTTAAACAGGACAGCTTCCATATCCACTCGCTT 1893  
Qy 540 TrpMetIleAspArgPheLeuPheGluValaSerGluAspValaArgArgProLeuGluVala 559  
Dh 1894 TGAATGAAGGTTTCTGTTTGGCTCTGTGAGGAAGACTTAAAGAGGCCACTGAGAGTCT 1953  
Qy 560 LeuLeuGluCysProValaProLeuGluValaIleGluIleLeuLeuHisIleThrValaSerLeu 579  
Dh 1954 CTGCTGGGCTGTCTCCCTTCCCTGCGGTGAACCAAGACTTGTGACTGGTCTGTCTG 2013  
Qy 580 LeuGluGlnIleProAsnAlaThrThrProGluValaSerThrLeuAspAlaPheHisCysLeu 599  
Dh 2014 TTGGGTCAAGACTTAATGACCAACCCAGAGACACCTTGACGCTTCCACTGTCTT 2073  
Qy 600 PheGluThrGlnAspLysGluPheValaArgLeuAlaLeuAsnSerPheGlnGluValaTrp 619  
Dh 2074 TTGAGACTCAAAACAAGAGTTTGTTCCTTGCAATTAACAGCTTCCAAAGAGTGTGG 2133  
Qy 620 LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysPro 639  
Dh 2134 CTTCGATTAAACCAAGACTGGACTTGATAGCATCTTCTTGTGCTCCAGCACTGTCCG 2193  
Qy 640 TyrLeuArgLysIleArgValaAspValaLysGluIlePheProArgAspGluSerAlaGlu 659  
Dh 2194 TATTTGGGAAAATTCCGGGTGATGTCAAAAGGATCTTCCAAAGATGAGTCCGCTGAG 2253  
Qy 660 AlaCysProValaValaProLeuTrpMetArgAspLysThrLeuIleGluGlnGlnTrpGlu 679  
Dh 2254 GCAATGCTGTGTGCTCTTATGATGCGGGAATGAAGCCCTCATTTGAGAGCACTGGGAA 2313  
Qy 680 AspPheCysSerMetLeuGluIleThrHisProHisIleuArgGluLeuAspLeuGluSerSer 699  
Dh 2314 GATTTCGTCTCATGCTTGGCAACCACTCACTGCGGAGAGCTGAGACCTCGGAGAGAC 2373  
Qy 700 IleuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisAspThrCysVala 719  
Dh 2374 ATCTGACAGAGCGGAGCTGAAGACCCTGTGTGCCAAGCTGAGAGCTCCACCTGCAAG 2433  
Qy 720 IleGlnThrIleuMetPheArgAsnAlaGlnIleThrProGluValaGlnHisIleuTrpArg 739  
Dh 2434 ATACAGACCTTGATTTAAATAATGACACAAATTAACCTCTGTGTGCAACCTCTGAGGA 2493  
Qy 740 IleValaMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGluGluIleThrHisIleLeuVala 759  
Dh 2494 ATGCTCATGGCCAAACCTTAACCTTAAGATCCCTCAACTTGGGAGGCAACCACTGAAGAA 2553



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QY 760 GluAspValArgMetAlaCysGluAlaLeuIleuYshisProlysCysLeuLeuGluSerLeu 779
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QY 780 ArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuIleuYshisSerGlnIleLeuThr 799
DB 2614 AGGCTGATGTCGTGGATGTAACCAATGCTGTACTGGAAGATCTCCAAATCTTACG 2673
QY 800 ThrSerProSerLeuYserLeuSerLeuAlaGlyValLeuYshisValThrArgGlnIleVal 819
DB 2674 ACCCTCCCAACCTGGAATCTGTGAGCTGAGAAACAAAGTGAACAGACAGGAGATA 2733
QY 820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnIleLeuIleuGln 839
DB 2734 AGGCTCTCAATGATGCTTGAAGGCTCTCCAGTCCGCTGCAAGACTGATCTGAG 2793
QY 840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
DB 2794 GACTGTGGCATCAACAGCAGGGTGGCAGAGTCTGGCCTCAGCCCTGTCAGCAACCGG 2853
QY 860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlyValLeuGlnIleValAsnLeu 879
DB 2854 AGCTTGACACACGTGTGCTTATCCAAACAGCTGGGAAACGAAGGTGAATCTACTG 2913
QY 880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
DB 2914 TGTGATCATAGAGCTTCCCACTGTAGTCTGCAAGAGGCTGATCTGAATCAGTCCAC 2973
QY 900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaMetGlyAsnSerTrpLeuThr 919
DB 2974 CTGAGCAGCGCTGGTGTGTCTCTTCTTCACTTGGCTTAACTGATGAGCTGACG 3033
QY 920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIleLeuLeuCysGlnVal 939
DB 3034 CACCTGACCTTGAAGATCAACCTGTGGAACGAATGCGTGAACCTTCTGTGCAAGTTC 3093
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DB 3094 ATGAGAGAACCATCTTGTCAATCTCCAGACCTGGAGTTGTGAATGTCAATCTCACGCC 3153
QY 960 AlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuIleYserLeuAsp 979
DB 3154 GCGTCTGTGAAGATCTGCTGCTGTGTGATCTGAGAGAGACACCTGAAGAGCTGGAT 3213
QY 980 LeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGlnIleLeuYshisGln 999
DB 3214 CTCAAGGACAAATGCGCTGGGTGAACGTGGGTGTGTGCTGTGTGAGAGGACCTGAAGCA 3273
QY 1000 LysAsnSerValLeuThrArgLeuGlyLeuIleValAlaCysGlyLeuThrSerAspCysCys 1019
DB 3274 AAGAACAGTGTCTGACAGACTCGGGTTGAAGGCAATGTGACTGATCTTGATTCCTGT 3333
QY 1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039
DB 3334 GAGGACACTCTCTTGGCCCTTTCTGCAACCGGCACTGACCAAGCTGAACCTGGAGCG 3393
QY 1040 AsnAsnPheSerProGlyGlyMetCysLeuCysSerAlaPheAlaCysProThrSer 1059
DB 3394 AATACTTCAGTCCCAAGGAATGATGAAGCTGTGTGCTGTGCTGTGCTGTGCTGTGCT 3453
QY 1060 AsnLeuGlnIleIleGlyLeuThrPheYshisTrpGlnIleYshisValIleArgYshisLeu 1079
DB 3454 AACTTACAGATTAATGGCTGTGGAATGCAAGTCACTGCTGCAATTAAGAACTGTGCTG 3513
QY 1080 GluGluValGlnLeuLeuYshisProArgValValIleAspGlySerTrpHisSerPheAsp 1099
DB 3514 GAGGAAGTGCAGCTCAAGCCCGAGTGTGAATTAAGAGCTAGTGGACTCTTTGAT 3573
QY 1100 GluAspAspArgHis 1104
DB 3574 GAAGATGACCGGTAC 3588

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RESULT 6

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US-10-399-443-23
; Sequence 23, Application US/10399443
; Publication No. US2004002869A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Alignment Scores:
Pred. No.: 0 Length: 3900
Score: 5741.50 Matches: 1098
Percent Similarity: 56.16% Conservative: 3
Best Local Similarity: 95.90% Mismatches: 3
Query Match: 81.16% Indels: 41
DB: 7 Gaps: 1

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QY 1 MetGluGlyAspIleYserLeuThrPheSerSerTyrGlyLeuGlnIleTrpCysLeuTyrGlu 20
DB 154 ATGGAAGAGCAAAATGCTCACCCTTTCCAGCTAAGGGCTGCAATGTGTCTCATAG 213
QY 21 LeuAspIleGluGluPheGlnIleThrPheYshisLeuLeuIleYshisSerSerGlnSer 40
DB 214 CTAGCAAGGAAGAAATTCAGACATTCAGAGAAATTAAGAAAGAAATTCAGAAATCG 273
QY 41 ThrThrCysSerIleProGlnPheGluIleGluAsnAlaAsnValGluCysLeuAlaLeu 60
DB 274 ACCACATCTCTATTCCAGAGTTGAATCGAAGATCGCAACGTGAAATGTCTGCATCTC 333
QY 61 LeuLeuHisGluTyrTyrGlyAlaSerLeuAlaTrpAlaTrpSerIleSerIlePheGln 80
DB 334 CTCTTGATGATGATTAATGAGCAATCGCTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTG 393
QY 81 AsnMetAsnLeuArgThrLeuSerGlyValAlaArgAspAspMetIleYshis----- 97
DB 394 AACATGAACCTGCGCAACCTCTCGGAGAAAGCAGCGGATGACATGAAGAAACATTCACCA 453
QY 97 ----- 97
DB 454 GAAGATCTGGAAGCAACATGATGACCAAGAACCAAGCAAGAAAGTCCAGAAAT 513
QY 98 -----115ser 99
DB 514 TCACAAAGTGTGCAACAAAGATAGTGCACAGCTGCAGAGACAAAGAACAGGAATTTCA 573
QY 100 GlnAlaMetGluGlnIleGlyValAlaThrAlaIleGluThrGluGlnIleSerGln 119
DB 574 CAAGCTATGGAACAAAGAGGTGCCACAGCAGAGAGAGAGAAAGAAATTTCAACA 633

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QY	120	AlAwetGluGlnGlnGluValAThValAlaGluThrGlnGlnGlnGlnValHISGlyValAsp	133
Db	634	GCTATGGAACAAGAGGTGGCCACAGCACAGAGACAGAAACAAGGACATGAGAGGTAC	693
QY	140	ThTTPAAspTYrLYsSerHisValMetThrLYsPheAlaGluGlnGluAspValArgArg	159
Db	694	ACATGGAGCTACAGAGATCACTGTATGACCAAAATTGGCTAGAGAGAGAGATGACCTGT	753
QY	160	SerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAlaGlyValaPheAsp	179
Db	754	AGTTTGAACCACTGCTGTGACTGGCCGGAATATGCAAAAGTTGGCTGTGCTTTGAT	813
QY	180	SerAspArgTrpGlyPheArgProArgThrValValaLeuHisGlyLYsSerGlyTLeGly	199
Db	814	TCAAGCCGGTGGGGCTTCGGCTCCGCTGCACGGGTGTTCACGGAAATGCAGAAATTGGG	873
QY	200	LYsSerAlaLeuAlaArgArgTLeValLeuCYsTrpAlaGlnGlyLYsLeuTYrGlnGly	219
Db	874	AAATGGGCTTACGCCAAGAGATCGTGTCTGGGGCAAGGTGACCTTACCAAGGA	933
QY	220	MetPheSerTYrValPhePheLeuProValArgGluMetGlnArgLYsLYsGluSerSer	239
Db	934	ATGTTCTCTACGTCTTCTTCTCCCGCTAGAGATGACGCGGAACAAGAGAGCAGT	993
QY	240	ValThrGluPheHISerArgLUTrpProAspSerGlnAlaProValThrGluTLeMet	259
Db	994	GTCAACAGAGTTCATCTCCAGAGAGGGCCAGACTCCACGGCTCCGGTACAGAGATCATYG	1053
QY	260	SerArgProGluArgLeuLeuPheTLeIleAspGlyPheAspAspLeuGlySerValLeu	279
Db	1054	TCCCAACCAAGAAAGCTGTGTGTTATCATATTGACGGTTTCAGATGACTGGGCTCTGTCTC	1113
QY	280	AsnAsnAspThrLYsLeuCYsLYsAspTrpAlaGlyLYsGlnProProPheThrLeuLe	299
Db	1114	AAACATGACACAAGACTCTGCAGAAACACTGGGGTGAAGAGAGCCTCCGTTACCCCTATA	1173
QY	300	ArgSerLeuLeuArgLYsValleuLeuProGluSerPheLeuTLeValThrValArgAsp	319
Db	1174	CGCACTCTGCTGAGGAGAGGTCTCTGCTCCCTGACTCTTCATGCTGCACCGTCAAGAAC	1233
QY	320	ValGlyThrGluLYsLeuLYsSerGlnValAlaSerProArgTYrLeuLeuValArgGly	339
Db	1234	GTGGGACAGAGAACTCAAGTCAGAGAGTGGTGTCTCCCGTTACTCTGTAGTTAGAGGA	1293
QY	340	ILeserGlyGlnGlnArgTLeHisLeuLeuLeuGlnArgGlyTLeGlyLYsHISGlnLYs	359
Db	1294	ATCTCGGGGAAACAAGATTCACATGCTCTTCTTGAGCCGGGATTGGTAGCATCAGAAAG	1353
QY	360	ThrGlnGlyLeuArgAlaTLeMetAsnAsnArgGlyLeuLeuAspGlnCYsGlnValPro	379
Db	1354	ACACAAAGGGTTGGCGCATCTCAACAACCGTGAAGCTGCACACATGGCCAGGTGGCC	1413
QY	380	AlaValGlySerLeuTLeCYsValAlaLeuGlnLeuGlnAspValValGlyGluSerVal	399
Db	1414	GGCGGGGCTCTCTATCTGCGGGCCCTTGACGCTGCAGAGAGTGGTGGGGAGAGCCTC	1473
QY	400	AlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThr	419
Db	1474	GGCCCTTCAACCAACGCTCACAGGCTGCACGCGCTTTGGCTTCAATCAGTCAACC	1533
QY	420	ProArgGlyValValArgArgCYsLeuAsnLeuGlnGluArgValValleuLYsArgPhe	439
Db	1534	CCTCAGAGCGTGGTCCGGCGGCTGTCTCAATCTGAGAGAAAGTTGTCTTGAAAGCGCTTC	1593
QY	440	CysArgMetAlaValGlnGlyValTTrpAsnArgLYsSerValPheAspGlyAspAspLeu	459
Db	1594	TGCCCTATAGCGGTGAGAGGAATGGAAATGAGATGATTGAATGTCAGCAACCTTC	1653
QY	460	MetValGlnGlyLeuGlyGluSerGlyLeuArgAlaLeuPheHisMetAsnTLeLeuLeu	479
Db	1654	ATGGTTCAAGAGCTCGGGAGAGTCTAAGCTCCGGTCTGTGTTCAATAAATCTCTTCTC	1713
QY	480	ProAspSerHisCYsGluGlnTyrTYrThrPhePheHisLeuSerLeuGlnAspPheCYs	499

Db	1714	CCAGACGACCACTGTGAGAGATACACACTTCTTCACCTCAAGTCCAGACTTCTGT	1772
QY	500	AlAlaIaLeuYrYrValIleuGluIyLeuGluIleGIuProAlaIeUcYsProIeUtyr	519
Db	1774	GCCGCTTGACTAGTGTAGAGGGCTGGAAATCGAGCAGACTCTGTGGCTCTGTAC	1833
QY	520	ValGluYrThrIlyrAlyrSerMetGluLeuYrGlnaGlyrPheHisIleHisSerIeu	539
Db	1834	GTTGAGAAAGCAAAAGAGGTCCATGAGCTTAAACAGGGAGGCTTCCATATCCACTGGCTT	1899
QY	540	TrpMetIlyrATrPheIeuPheGIyLeuValSerGIuAspValArgArProIeuGIuVal	559
Db	1894	TGGATGAAGCTTTCTTGTGTGGCTCGTGAACCAAGACGTAAGAGGCCACTGGAGGT	1955
QY	560	LeuIeuGIyCysProValProIeuGIyValIySGluYleuLeuHisITryValSerIeu	579
Db	1954	CTGCTGGGCTGTCCCGTTCCTCCGGGGGTGAAGCAGAAAGCTTTCGCACTGGAGTCTCTGTG	2013
QY	580	LeuGIyGIuGIuIleProIeuAlaThrThrProGIyAspThrIleuAspAlaPheHisSerIeu	599
Db	2014	TTGGGTCCAGCAGCCTTAATGACCAACCCACAGAGACACCTCGAAGGCTTCCACTGTCTT	2077
QY	600	PheGIuThrGIuAspIlyrGIuPheValArgIeuAlaIeuAsnSerPheGIuGIuValITrp	619
Db	2074	TTTCAGACTCCAAAGCAAAAGATTGTTCGTCTGGCATTTAAACGCTTCCAAAGACTGTGG	2133
QY	620	LeuProIleuGIuIleAsnIleuAspIleuIleAsnSerPheCysLeuGIuIleIyCysPro	639
Db	2134	CTTCGCAATTAAACGAACCTGGAAGTTGATAGATCTTCTCTGCGCTCAGAGACTGTCCG	2199
QY	640	TyrIleuArgIlyrIleArgValAspValIySGlyIlePheProIyAspGIuSerIleuIleu	659
Db	2194	TATTTGGCGAAATATTCGGGTGAGTCCAAAGGATCTTCCAAAGAGATGAGTCCGCTGAG	2255
QY	660	AlaCysProValIleProIeuTrpMetArgAspIlyrThrIleuIleGIuGIuITrGIu	679
Db	2254	GCATGTCTGTGTCTCTTAAGATGGGGATTAAGACCTTCATTGAAGAGCAGTGGAA	2311
QY	680	AspPheCysSerMetIleuGIyThrHisProHisIleuArgIleuAspIleuGIySerSer	699
Db	2314	GATTTCTGTCTCAATGCTTGGCACCAACCAACCTGGGGCAGCTGGAAGCTGGCAGCAGC	2372
QY	700	IleIeuThrGIuArgAlaMetIlyrThrIeuCysAlaIyIleuArgHisProThrCysIyIy	719
Db	2374	ATCTCGACAGAGCGGGCCATGAAGAAGCCTGTGTGCAAGCTGAAGGCATCCCACTGGCAG	2433
QY	720	IleGIuIThrIleuMetPheArgAsnAlaGlnIleIThrProGIyValGIuHisIleuITrArg	739
Db	2434	ATACGACCCCTGATGTGTTAAGAAAGCAAGATTACCTCTGTGTGCAACCTCTGGAGA	2499
QY	740	IleValIleMetAlaAsnArgAsnIleuArgSerIleuAsnIleuGIyGIyThrHisIleuIyGIu	759
Db	2494	ATTCGTCAAGGCCAACCGTAACCTTAAGATCCCTCAACTTGGGAGGCCAACCACTGAAGGA	2555
QY	760	GIuAspValAlaGmetAlaCysGIuAlaIleuIyHisProIyIyCysIleuIeuGIuSerIeu	779
Db	2554	GAGGATGTAAAGGATGGCGTGAAGCCTTAAACACCCCAAAATGTTGTGTGAAGTCTTGG	2613
QY	780	ArgIleuAspCysCysGIyIleuThrHisAlaCysITryIleuIyHisIleSerGIuIleuIThr	799
Db	2614	AGGCTGAATGCTGTGAATTAACCATCTGTATACCTGAAGANTTCCAAATCTTACG	2677
QY	800	ThrSerProSerIleuIySerIleuSerIleuAlaGIyAsnIyIyValIThrAspGIuGIuVal	819
Db	2674	ACCTTCCCCAGCTGAATCTCTGAGCTCTGGCAGGAACAAAGTACAGACCAAGGAGTA	2733
QY	820	MetProIeuSerAspAlaIleuArgValSerGIuIyCysAlaIeuGIuIyIleuGIuIleuGIu	839
Db	2734	ACGCTCTCAAGAGAGCTTGAAGGCTGCCAGTGCCTGGCAGAACTGATATCTGGAG	2799
QY	840	AspCysGIyIleIThrAlaThrGIyCysGIuSerIleuAlaSerAlaIleuValSerIlyrArg	859

Db	2794	GACGTGGCATTACAGACGCAAGGGTTTGCAGAGTCTGGCTCAGACCCCTGTCAGCAACCGG	2853
Qy	860	SeLeuthrthiSLeuCySLeuSerAAsnSerLeuGlyAAsnGlyValAAsnLeuLeu	879
Db	2854	AGCTTGCACACCTGTGCTTATCCAAACAGCCCTGGGAAACGAAGGTGAATCTACTG	2913
Qy	880	CyAAsrSerMetCAsrLeuProHicCyAsrSerLeuGlnAsgLeuMetLeuAAsnGlnCyHicS	899
Db	2914	TGTGCATTCATGAGGGCTTCCCACTGTAGTCTGCAGAGGCTGATCTGAATCATGGTCCAC	2973
Qy	900	LeuAAsrThrAlaGlyCySLeuPheLeuAlaLeuAlaLeuMetGlyAAsrSerTrpLeuThr	919
Db	2974	CTGCAGACGGCTGGCTGTGTCTCTTTCACATTTGGCTTAATGGGTAACTGAATGCTGACG	3033
Qy	920	HisLeuSerLeuSerMetAAsnProValGluAAsnGlyValAAsnLeuCySLeuVal	939
Db	3034	CACCTGAACCTTTAGCATGAACCTTGTGAAGACAAATGCGGTGAACCTTGTGCGCAAGGTC	3092
Qy	940	MetAAsrGluProSerCyHicSLeuGlnAAsrLeuGlyLeuValAAsnCyHicSLeuThrAla	959
Db	3094	ATGAGAGAACCAATCTTGTATCTCCAGACCTGGAGTTGTAAATGTATCATCTCACCGCC	3155
Qy	960	AlaCySAsrGluSerLeuSerCyValIleSerAAsrSerAAsrGhiSLeuAAsnSerLeuAAsr	979
Db	3154	GCGTCTGTGAAGAGTCTGTCTCTGTGTATCTGCAGAGACAGACACTGAAGAGCTGGAT	3213
Qy	980	LeuThrAAsnAAsnAlaLeuGlyAAsrGlyValAlaAlaLeuCySLeuGlyLeuAAsnGln	999
Db	3214	CTCACGGAACAATGCCCTGGGTGACGCTGGGGGTGTGCTGGCTGTGCGAGGGACTGAAGCA	3272
Qy	1000	LyAAsnSerValLeuThrAAsrLeuGlyLeuAAsnGlyAAsnGlyLeuThrSerAAsrCyS	1015
Db	3274	AAGAACAGGTGTTCTGACAGACATCTCGGTGAAGGAGATGAGACTGACTGATTAATGCTGT	3333
Qy	1020	GluAlaLeuSerLeuAlaLeuSerCyAAsnAAsrGhiSLeuThrSerLeuAAsnLeuValGln	1033
Db	3334	GAGGCACTCTCTTGGCCCTTTCTCTGCAACCGGCACTGACCAAGCTTAACCTGGTGCAG	3392
Qy	1040	AAsnAAsnPheSerProAAsrGlyMetMetCysLeuCySAsrAlaPheAlaCyAAsrProThrSer	1055
Db	3394	AATAACTTCAGTCCCAAGGAATGATGAAGCTGTGTGGGCTTTGCTGCTCCACAGTCT	3453
Qy	1060	AAsnLeuGlnIleIleGlyLeuTrpAAsrGlnTrpProValGlnIleAAsrGlyLeuLeu	1077
Db	3454	AACCTTACAGTAAATTTGGGTGTGGAAATGGCAGTACCCCTGTCAAAATAGGAAGCTGCTG	3511
Qy	1080	GluGluValAlaGlnLeuLeuAAsrProAAsrValAlaIleAAsrGlySerTrpHisSerPheAAsr	1099
Db	3514	GAGGAAGTGCACCTACTCAAGCCCGAAGTGTGAATTAACGATGATTGGCAATCTTTGAT	3572
Qy	1100	GluAAsrAAsrAAsrGhiS 1104	
Db	3574	GAAAGTGAACCGGTAC 3588	
RESULT 7			
US-10-677-943-23			
; Sequence 23, Application US/10677943			
; Publication No. US20040072297A1			
GENERAL INFORMATION:			
; APPLICANT: The Government of the United States of America as			
; APPLICANT: represented by the Secretary of the Department of Health and			
; APPLICANT: Human Services			
; APPLICANT: Nelson, Lawrence			
; APPLICANT: Tong, Zhi-Bin			
TITLE OF INVENTION: Human Gene Critical to Fertility			
; FIDE REFERENCE: 4239-64790			
CURRENT APPLICATION NUMBER: US/10/677,943			
CURRENT FILING DATE: 2003-10-01			
PRIORITY APPLICATION NUMBER: 60/241,510			
PRIORITY FILING DATE: 2000-10-18			
PRIORITY APPLICATION NUMBER: PCT/US02/09776			
PRIORITY FILING DATE: 2002-03-29			
PRIORITY APPLICATION NUMBER: PCT/US01/10981			

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; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
US-10-677-943-23

Alignment Scores:
Pred. No.: 0
Score: 5741.50
Percent Similarity: 96.16%
Best Local Similarity: 95.90%
Query Match: 81.16%
DB: 7

Length: 3900
Matches: 1098
Conservative: 3
Mismatches: 3
Indels: 41
Gaps: 1

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QY	21	LeuAaPlySGIuGIuPheGInThrPhePlySGIuLeuLeuLYSLeuYSerSerGIuSer	40
Db	214	CTAGCAAGAGAAATTTTCAGACATTCACAGAAATTACTAAAGAGAAATCTTCAGATCG	273
QY	41	ThrThrCysSerLLeuProGlnPheGluIleGIuAsnAlaAsnValGluCysLeuAlaLeu	60
Db	274	ACCAATGCTCTATTCACACAGTTTAAATCGAAGATCGCAACGCTGGAATGCTCGACATC	333
QY	61	LeuLeuHISGIuTYRTrpGIYValaSerLeuAlaTrpAlaThrSerLLeuSerLLeuPheGlu	80
Db	334	CTCTTGCAAGATATTATGAGACATCGCTGGGCTTGAGCTACGTCATTACATCTTTGAA	393
QY	81	AsnMetCAsnLeuAaTYRThrLeuSerGIuYValaArgAspAspMetLYSLeuYSer	97
Db	394	AACATGAACCTCGGAACCTCTCGGAGAAAGGACGGGATGACATGAAGAACAATTCCCA	453
QY	97	-----	97
Db	454	GAAGATCTGAAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTCCAGAAATT	513
QY	98	-----IleSer	99
Db	514	TCACAAGCTGTGCACACAGATAGTCCACACCTGCGAGAGACAAAAGACAGGAATTTCA	573
QY	100	GlnAlaMetGIuGIuGIuGIYValaThrAlaAlaGIuThrGIuGIuGIuIleSerGln	119
Db	574	CAGCTATGGAACACAGAGAGTCCACAGACGACAGACACAGAAACAAGAAATTTCCAA	633
QY	120	AlaMetGIuGIuGIuGIYValaThrAlaAlaGIuThrGIuGIuGIuGIYHISGIYGIYAsp	139
Db	634	GCTATGGAACAGAGAGTCCACAGACGACAGACAGAAAGAACAGGACATGAGAGGTGAC	693
QY	140	ThrTrpAspTYRLeuSerHISValMetThrLYSPhaAlaGIuGIuGIuAspValArgArg	159
Db	694	ACATGGAGACTACAGAGTCACTGAGTGAACCAATTCGCTGAGGAGGAGATGACGTGCT	753
QY	160	SerPheGluAsnThrAlaAlaAspTrpProGluMetGIuThrLeuAlaGIYAlaPheAsp	179
Db	754	AGTTTGGAAAAACATCTGCTGACTGCGCGGAAATCCAAACGTTGGCTGGTCTTTGAT	813
QY	180	SerAspArgTrpGIYPhaArgProArgThrValValLeuHISGIYLYSLeuSerGIYIleGIY	199
Db	814	TCAGACCGGTGGGCTTCCGGCTCGCACAGGTGTCTTGACCGGAAAGTCAGGAATTTGGG	873
QY	200	LYSLeuAlaLeuAlaArgArgIleValLeuCysTrpAlaGIuGIuGIYLeuTYRGIY	219
Db	874	AAATGGGCTCTAGCCAGAAAGATCGCTGTGTGGGCGCAAGGTGATCTTACAGGGA	933

Qy 220 MetPheSerTyrValPhePheLeuProValArgGluMetGluArgGlySlySerSer 239  
Db 934 ATGTTCTCCACAGCTCTTCTCTCCGTTAGAGAGATGCAAGCGGAGAGAGAGAGAGCT 993  
Qy 240 ValThrGluPheIleSerArgGluTyrProAspSerGluAlaProValThrGluIleMet 259  
Db 994 GTCAAGAGATTCACTCCAGAGAGATGCGCAGACTCCAGAGCTCCGCTGAGACGAGATCATG 1053  
Qy 260 SerArgProGluArgLeuPheIleIleAspGlyPheAspAspLeuGlySerValLeu 279  
Db 1054 TCCGACCAAGAAAGGCTGTGTTGATCATGACGGTTTCAGATGACCTGGGCTGTCTCTC 1113  
Qy 280 AsnAsnAspThrIlySleuCySlyAspTyrAlaGluSylProProPheThrLeuIle 299  
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Qy 300 ArgSerLeuLeuArgGlyValLeuLeuProGluSerPheLeuIleValThrValArgAsp 319  
Db 1174 CGCAGTCTGCTGAGAGAGATCTGCTCTCCAGAGCTCTTCTGATCTGACCCGCTCAGAGAC 1233  
Qy 320 ValGluThrGluSylSleuLeuSerGluValValSerProArgTyrLeuLeuValArgGly 339  
Db 1234 GTGGGCAAGAGAGAGCTCAAGTCAAGAGTGTCTCCGTTACCTGTTAGTGAAGA 1293  
Qy 340 IleSerGlyGluGluArgIleHisLeuLeuLeuGluArgGlyIleGlyGluHisGluSyls 359  
Db 1294 ATCTCGGGGAGAACAAATCCACTTGTCTTGAAGCGGGAGATGGTGAAGCATCAAGAG 1353  
Qy 360 ThrGluGlyLeuArgAlaIleMetAsnAsnArgGluLeuLeuAspGluGluValPro 379  
Db 1354 ACAAGAGGTTGCGTGTGATCATCAACACCGTGAAGTGTCTGACGAGTGCAGAGTCCC 1413  
Qy 380 AlaValGlySerLeuIleCySlyAlaLeuGluLeuGluAspValValGlyGluSerVal 399  
Db 1414 GCGGTGGGCTCTCTCATCTGTGTGGTCCAGCTGACGAGAGTGTGGGGAGAGAGCTC 1473  
Qy 400 AlaProPheAsnGluThrThrGluLeuHisAlaAlaPheValPheHisGluLeuThr 419  
Db 1474 GCCCCTTCAACCAACGCTCAAGGCTGACAGCGCTGTCGTTGCTTCAATCAGCTCACC 1533  
Qy 420 ProArgGlyValValArgArgCySlyLeuAsnLeuGluGluArgValValLeuValArgPhe 439  
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Qy 460 MetValGluGlyLeuGlyGluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeu 479  
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Qy 480 ProAspSerHisCySylGluGluTyrTyrThrPhePheHisIleuSerLeuGluAspPheCyS 499  
Db 1714 CCGAGACGCACTGTGAGAGTACTACACTTCTTCCACCTCACTTCCCGAGACTTCTGT 1773  
Qy 500 AlaAlaLeuTyrTyrValIleuGluGluLeuGluIleGluProAlaLeuCySProLeuTyr 519  
Db 1774 GCGGCTTGTACTACGTTATAGAGAGGCTTGGAATCCAGCCAGCTTCTTGGCTCTGTAC 1833  
Qy 520 ValGluSylThrIlyAspSerMetGluLeuSylGluAlaGlyPheHisIleHisSerLeu 539  
Db 1834 GTTGAGAGAGCAAAAGAGTCTCATGAGCTTAAACAGGAGGCTTCCATATCACTCGCTT 1893  
Qy 540 TyrMetIlyAspPheLeuPheGlyLeuValSerGluAspValAlaArgArgProLeuGluVal 559  
Db 1894 TGGATGAAGGGTTTCTTGTGTGCTGTGTGAGCAAAAGATTGAAGAGAGAGAGAGAGAG 1953  
Qy 560 LeuLeuGlyCySProValProLeuGlyValIlySylGluSylLeuLeuHisIleTyrValSerLeu 579  
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Qy 580 LeuGlyGluGluProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCySLeu 599  
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Qy 620 LeuProIleAsnGluAsnLeuAspLeuIleAlaSerSerPheCySLeuGluHisCySPro 639  
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Qy 660 AlaCySProValValProLeuTyrMetArgAspIlyThrLeuIleGluGluGluGlu 679  
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Qy 800 ThrSerProSerLeuIlySerSerLeuAlaGlyAsnIlyValThrAspGluIlyVal 819  
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Qy 820 MetProLeuSerAspAlaLeuArgValSerGluCySAlaLeuGluIlySylLeuGlu 839  
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Qy 840 AspCySylIlyThrAlaThrGlyCySylGluSerLeuAlaSerAlaLeuValSerAspArg 859  
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Qy 860 SerLeuThrHisLeuCySLeuSerAsnAsnSerLeuGlyAsnGluIlyValAsnLeuLeu 879  
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Qy 900 LeuAspThrAlaGlyCySylPheLeuAlaLeuAlaLeuMetGlyAsnSerTyrPheThr 919  
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Qy 920 HisLeuSerLeuSerMetAsnProValGluAspAsnGlyValIlySylLeuLeuCySylVal 939  
Db 3034 CACTGAGCTTATGACATGAACCTGTGAGAGAGACATGAGCGTGAAGCTTCTGTGAGAGTGC 3093  
Qy 940 MetArgGluProSerCySHisIleuGluAspLeuGluLeuValIlyCySHisIleuThrAla 959

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Db      3094 ATGAGAACCATCTTGTCACTCCAGGACCTGGAGTTGTAAGTGCATCTCACCGCC 3153
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Db      3154 GCGGTGCTGTGAGAGTCTGTCTGTGTGTATCTCGAGAGCACACCTGAAAGACCTGGAT 3213
Qy      980  LeuThrAspAsnAlaLeuGlyAspGlyGlyValAlaAlaLeuCyseGluGlyLeuLysGln 999
Db      3214 CTCACGACAAATGCGCTGGGTGACGAGTGGAGTTGCTGCGCTGCGAGGAGCTGAGCA 3273
Qy      1000 LysAsnSerValLeuThrArgLeuGlyLeuLysAlaCyseGlyLeuThrSerAspCyse 1019
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Qy      1020 GluAlaLeuSerLeuAlaLeuSerCyseAsnArgHleuThrSerleuAsnLeuValGln 1039
Db      3334 GAGGACCTCTCTCTGCGCTTCTCTGCAACCGGACATCGACAGCTAAACCTGGTGAG 3393
Qy      1040 AsnAsnPheserProLysGlyMetMetLysLeuCyseSerAlaPheAlaCyseProThrSer 1059
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Qy      1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTrpProValGlnIleArgLysLeuLeu 1079
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Qy      1080 GluGluValGlnLeuLeuLysProArgValValIleAspGlySerTrpHisSerPheAsp 1099
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Qy      1100 GluAspAspArgHis 1104
Db      3574 GAAGATGACCGGTAC 3588

RESULT 8
US-10-216-645-3
; Sequence 3, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAEL
; APPLICANT: BECKMANN, GREGG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-645-3

Alignment Scores:
Pred. No.: 0 Length: 3830
Score: 5683.50 Matches: 1087
Percent Similarity: 95.87% Conservative: 5
Best Local Similarity: 95.43% Mismatches: 12
Query Match: 80.34% Indels: 35
DB: 6 Gaps: 2

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Qy      21 LeuAspLysGluGluPheGlnThrPheLysGluLeuLysLysSerSerSerGluSer 40

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Qy      41 ThrThrCyseSerIleProGlnPheGluIleGluAsnAlaAsnValGluCyseLeuAlaLeu 60
Db      121 ACCAATGCTCTATTCACAGTTTGAAATTCAGAAATTCAGAAATTCAGAAATTCAGAAATTC 180
Qy      61 LeuLeuIleGluTrpGlyValaSerLeuAlaTrpAlaThrSerIleSerIlePheGlu 80
Db      181 CTCTTGATAGATGATTTAGAGATCGCTGGCTGGGCTAGTCAATAGCATCTTTGAA 240
Qy      81 AsnMetAsnLeuArgThrLeuSerGluLysAlaArgAspMetLysLysIleSerGln 100
Db      241 AACATGAACCTGCGAACCTCTCGAGAGAGGACAGGAGTGCATGAAATAATTCACAGAA 300
Qy      101 -----AlaMetGluGlnGluGlyValaThrAlaIleGluGlnGluGln--- 115
Db      301 GATCCTGAAGACAGATGACTGACCAAGACCAAGCAAGAAAGAAAGTCCGAAATAATA 360
Qy      115 ----- 115
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Qy      116 -----GluIleSerGlnAlaMetGluGlnGluGly 125
Db      421 AAGTATGTTGGAATTCATCTTCTTTGCAAGAAATTCACAAAGCTATGGAACAAAGAGT 480
Qy      126 AlaThrAlaIleGluThrGluGluGlnGlyIleGlyValaAspTrpTrpAspTrpLysSer 145
Db      481 GCCACAGAGAGAGACAGAAAGAAACAGACATGAGGTGACACATGAGGACTTACAGAGT 540
Qy      146 HisValMetThrLysPheAlaGluGluLysAspValArgArgSerPheGluAsnThrAla 165
Db      541 CACGTGATGACCAAAATTCGCTGAGAGAGAGATGATGATGATTTTGAAGAAACATCTCT 600
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Qy      186 ArgProArgThrValValLeuHisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArg 205
Db      661 CGGCTTCAGCGGTGTTCTCACGAAAGTCAGAAATGGAATCGGCTCTACCGCA 720
Qy      206 ArgIleValLeuCyseTrpAlaGlnGlyGlyLeuTrpGlnIleMetPheSerTrpValPhe 225
Db      721 AGGATCGTGTGTGTGGGCCCAAGTGCATCTACAGGAAATGTTCTCTAGGTCTTC 780
Qy      226 PheLeuProValaArgLysMetGlnArgLysGluSerSerValThrGluPheIleSer 245
Db      781 TTCCTCCCGTTAGAGATGACAGGAAAGAGAGACATGTCACAGAGTTCATCTCC 840
Qy      246 ArgGluTrpProAspSerGlnAlaProValaThrGluIleMetSerArgProGluArgLeu 265
Db      841 AGGAGTGGCCAGACTCCAGAGCTCCGGTGAAGAGATCAATGCCGACAGAAAGGCTG 900
Qy      266 LeuPheIleIleAspGlyPheAspAspLeuGlySerValLeuAsnAspAspThrLysLeu 285
Db      901 TTGTTTCATTTGACGGTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy      286 CysLysAspTrpAlaGluLysGlnProProPheThrIleuIleArgSerLeuLeuArgLys 305
Db      961 TGCAAAAGACTGGGCTGAGAAACAGGCTCGTTTCAACCTCATACGACATCTGTGAGAG 1020
Qy      306 ValLeuLeuProGluSerPheLeuIleValaThrValaArgAspValGlyThrGluLysLeu 325
Db      1021 GTCTGCTCTCTGAGTCTTCTTATGTCACCGTCAGACAGAGTGGGACAGAGAGGCTC 1080
Qy      326 LysSerGluValaLysProArgTrpLeuLeuValaArgGlyIleSerGlyGluGlnArg 345
Db      1081 AAGTCAGAGTGTGTCTCCCGTTACTGTTAGTAAAGAAATTCGCGGGAACAAAGA 1140
Qy      346 IleHisLeuLeuGluLysArgGlyIleGlyLysHisGlnLysThrGlnGlyLeuArgAla 365

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Db 1141 ATCCACTGTCCTTGAGCGCGGATTGTGAGCATCAGAAAGACACAGGGTTGCGTCCG 1200  
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Db 1201 ATCATGAACAACCGTAGCTGCTGACACAGTGCAGAGTCCCGCGGCTCTCTATC 1260  
Qy 386 CysValAlaLeuGlnLeuGlnAspValValGlyGlySerValAlaProPheAsnGlnThr 405  
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Qy 466 GluSerGluLeuArgAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisLeuGlu 485  
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Qy 506 LeuGlnGlyLeuGlnIleGluProAlaLeuCysProLeuTyrValGluTyrThrLysArg 525  
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Qy 526 SerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTyrMetLysArgPheLeu 545  
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Qy 546 PheGlyLeuValSerGluAspValArgArgProLeuGlnIValLeuLeuGlyCysProVal 565  
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Db 1801 CCCCTGGGGGTGAAGCAGAAGCTTCTGCACCTGGGCTCTCTGTGGGTCAAGCACTGAAT 1860  
Qy 586 AlaThrThrProGlyAspThrLeuAspAlaPheHisGlyCysLeuPheGlnThrGlnAspLys 605  
Db 1861 GCCACCAACCCGAGAGACACCTGTGAGCGCTTCCACTGTCTTTCAGAGACTCAAGACAAA 1920  
Qy 606 GluPheValArgLeuAlaLeuAsnSerPheGlnGlnIValTTrpLeuProIleAsnGlnAsn 625  
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Qy 626 LeuAspLeuIleAlaSerSerPheCysLeuGlnHisCysProTyrLeuAspLysIleArg 645  
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Qy 646 ValAspValLysGlyIlePheProArgAspGlnSerAlaGlnAlaCysProValValPro 665  
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Qy 666 LeuTTrpMetArgAspLysThrLeuIleGlnGlnIleGlnTTrpGluAspPheCysSerMetLeu 685  
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Qy 686 GlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAla 705  
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Db 2221 ATGAAGACCCGTGTGTGCCAAGCTGAGGATCCCACTGCAAGATTAAGACCTGTATGTTT 2280

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Qy 1026 LeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGlnAsnAsnPheSerProLys 1045  
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Oy      1086  ysyphroahgva1valli1eapxg1setrthiisecrheapgiuapapapcgh1e 1104
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RESULT 9
US-10-092-900A-347
; Sequence 347. Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol R.A.
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patnurajan, Meera
; APPLICANT: Gangoli, Bsha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandez, Elma R.
; APPLICANT: Caeman, Stacie J.
; APPLICANT: Malyskar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Albrobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT FILING DATE: US/10/092,900A
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 347
; LENGTH: 3226
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(3168)

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Db 1073 CGCCGCTTGTGTTCATCAGCTCACCTCGAGGGGTGGTCCGGGTGTCTCAATCT 1132  
Qy 430 UGIUGIARGVAIALEUHSARGPHECYBARGMETALVAIGIUGIYVAITRPAENAR 450  
Db 1133 GAGGAAAGAGTTGTCTGAAAGCCCTTCTGCCGATATGGCTGTGAGGAGATGTGGAAATAG 1192  
Qy 450 GLYSERVALPHEASPGIYASPAAPLEUMETVALGINGIYLEUGIYGIUSERGIUEUAR 470  
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Qy 490 EPHEHISLEUSERLEUGINAPHECYBALAIALEUTYTYVAIALEUGIYLEUGI 510  
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Qy 550 RGIUAERVALARGARGPROLEUGIUAIALEULEUGIYASPROVALPROLEUGIYVAL 570  
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Qy 570 SGINLYLEUENHISITRVALSERLEULEUGIYGLINLEUPROASNAATHRTHPROGI 590  
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Qy 930 PARGNGIYVALYLEULEUCYSGIUAIALEUATARGIUPROSECYSHISLEUGINAPLE 950  
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Qy 950 UGIULEUVALYCYSHISLEUTHRALAIAICYCYSGIUSERLEUSERCYVALIIESE 970  
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Qy 1050 UCYSESERIALPHEALACYSPROTHRISERANLEUGINILIEGLIYEURTPYSTPRGI 1070  
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RESULT 10  
US-10-339-443-5  
; Sequence 5, Application US/10399443



Publication No. US20040028669A1  
 GENERAL INFORMATION:  
 APPLICANT: The Government of the United States of America, as Represented by the  
 APPLICANT: Secretary, Department of Health & Human Services, The National Institute  
 APPLICANT: Health  
 APPLICANT: Nelson, Lawrence M.  
 APPLICANT: Tong, Zhi-Bin  
 APPLICANT: Nelson, Lawrence  
 APPLICANT: Zhi-Bin, Tong  
 TITLE OF INVENTION: Human Gene Critical to Fertility  
 FILE REFERENCE: 4239-64785  
 CURRENT APPLICATION NUMBER: US/10/399,443  
 CURRENT FILING DATE: 2003-04-16  
 PRIOR APPLICATION NUMBER: 60/241,510  
 PRIOR FILING DATE: 2000-10-18  
 PRIOR APPLICATION NUMBER: PCT/US01/10981  
 PRIOR FILING DATE: 2001-04-04  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 5  
 LENGTH: 3447  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-10-399-443-5

Alignment Scores:  
 Pred. No.: 1.37e-275 Length: 3447  
 Score: 2688.00 Matches: 554  
 Percent Similarity: 66.49% Conservative: 186  
 Best Local Similarity: 49.78% Mismatches: 293  
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 Gaps: 11

US-10-066-521-6 (1-1344) x US-10-399-443-5 (1-3447)

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Qy 55 ValGluCyLeuAlaLeuLeuLeuHileGluTYrTYrGlyAlaSerLeuAlaIrrPaIaThr 74
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Qy 75 SerIleSerIlePheGluAaMetAaLeuAaIrrPaIaSerGluLeuAlaIrrPaIa 94
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Qy 95 MetLysLysIleSerGln----- 100
Db 300 GTGAAACAGGGGTCAAGAAATGAATCTTCTCAGAAACAGACAGTAAATCAATCCAG 359
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Db 420 GAAGTCAAGAGCA-----GATAAAGT 443
Qy 136 HisGlyGlyAaPheThrTTPAaPheTYrLysSerHisValMetThrLysPheAlaGluGlu 155
Db 444 AATGAGGTGACTTCAAGACTAAGAGCCCATGTGATGCTTAAGTTCACACCAAGTGG 503
Qy 156 AspValaLysArgSerPheGluAaSerHisAlaIleAaPheTTPProGluMetGlnThrLeu 175
Db 504 GATTCACAC-----TATGACAGCCCAAGATGAAATTAATGATGCT 542
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QY 593 LeuAspAlaPheHisCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeu 612
Db 1791 CTGAGTGCCTTCAATGCTTAATTTGAGCTCAGAGATAAGAGTTTGTGCGGGGCTCTC 1850
QY 613 AsnSerPheGlnGluValTrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSer 632
Db 1851 AAACGCTCCAAAGAGTGTGGCTGCTGATTAACCAAGAAATGACCTTGAAGTCTCTTCC 1910
QY 633 PheCysLeuGlnHisCysProGlyLeuArgLysIleArgValAspValLysGlyIlePhe 652
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QY 1092 AspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
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RESULT 11
US-10-677-943-5
; Sequence 5, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; represented by the Secretary of the Department of Health and
; Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677, 943
; CURRENT FILING DATE: 2003-10-01, 510
; PRIOR APPLICATION NUMBER: 60/241, 510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 3447
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-677-943-5

Alignment Scores:
Pred. No.: 1,37e-275 Length: 3447
Score: 2688.00 Matches: 554
Percent Similarity: 66.49% Conservative: 186
Best Local Similarity: 49.78% Mismatches: 293

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Query Match:	38.00%	Indels:	81
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US-10-066-521-6 (1-1344) x US-10-677-943-5 (1-3447)			
QY	15	GIITRTPCYsLeuTYRGluLeuAspLyseGluInpHeGlnThrPheLySGluLeuLeuLyS	34
DB	163	CAATGGGCTCCCA-GAAAAAGACAGTAAGAACATCTTGAAGACGCGATTTGGAAAG	221
QY	35	LySlySerSerGluSerThrThCySerSerLeProGlnPheGluIleGluAsnAlaSn	54
DB	222	GAACAGAGTCCAGAAAGCACA-----	242
QY	55	ValGluCySLeuAlaLeuLeuLeuHiegluTYRtyrGlyAlaSerLeuAlaTrpAlaThr	74
DB	242	-----	242
QY	75	SeRleSerIlePheGluAsnMetAsnLeuArgThrLeuSerGluLyAlaArgAspAsp	94
DB	243	---ATGTCCTCTTCAGAAATATGTCAGTAGACCAATCTTGAAGACAGTGATCAGAAAGA	299
QY	95	MethylValylSerGln-----	100
DB	300	GTGGAACAGCGCTCAGAAAGAAATGCACTTCCAGAAACGACAGTAATCAATCCAG	359
QY	101	-----AlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln	115
DB	360	AAAGACCAAGACCAAGACAGAGACGACGACATCAGAAACCTTCAATCTTAAGAAAGAGAT	419
QY	116	GluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGlnGly	135
DB	420	GAAAGACAGAGGCA-----	443
QY	136	HiSeGlyGlyAspThrTPAspTYrLyseSerHieValMetThrLyPheAlaGluGluGlu	155
DB	444	AATGAGGTGACTTACAGAGCTTACAGAGCCCATGTGATGTCTAAGTTCTGCACAAAGTGTG	503
QY	156	AspValaArgAspSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla	175
DB	504	GATCTACAC-----TATGACAGCCCGAGATGAATAATTATGTCT	542
QY	176	GlyAlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeuHieGlyLyS	195
DB	543	GATGCTTTAAACCATACCAAGAAACCTTCCAGCCTCACACATATCTCTCATGGAAGA	602
QY	196	SerGlyIleGlyLyseSerAlaLeuAlaArgArgIleValLeuGlySerTrpAlaGluGlyGly	215
DB	603	CCAGAGATGGGAAATCAGCTTTGGCCAGAAAGTATTTGTTGGCTGGGCACAGGGTAA	662
QY	216	LeuTYRGlnGlyMetPheSerTYrAlaPhePheLeuProValArgGluMetGlnArgLyS	235
DB	663	CTCTTCCAAAAATG---TCTTTGTCACTCTTCTCTGTTAAGAAATAAAGTGACCA	719
QY	236	LyseGluSerSerValThrGluPheIleSerArgGluTYrProAspSerGlnAlaProVal	255
DB	720	GAGAAAGACAGATTGGCACAAGCTGATTTGCTAAGAGGTGTCCAGACTCTCGGAGATCTAGTG	779
QY	256	ThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAspLeu	275
DB	780	ACAAAGATCATGTCCCAACAGAAAGACTCTTGTTGTCTAAGATAGGCTTGGAGATATAG	839
QY	276	GlySerValLeu---AsnAsnAspThrLySLeuCyLySAspTrpAlaGluLyseGlnPro	294
DB	840	GACTGTGCTCTCAACATGATGATATGACATATCCAGAGACTGGAAGATGAACAGCC	899
QY	295	ProPheThrLeuIleArgSerIleuArgLyValLeuLeuProGluSerPheLeuIle	314
DB	900	ATATCATCTCGATGTACAGCTCTCTGAGAGAGGCTCTTCACTCACTCACTCTTCTCATC	959
QY	315	ValThrValArgAspValGlyThrGluLySLeuLySergluValValSerProArgTYR	334
DB	960	ATTACACCAAGAAACAGGCTTTAAGAAATCACTCAAGTCAATGTTGTGTCTCCCTCAT	1019

QY	335	LeuLeuValAaGgLyIleSeGgLyVgIgLgIaPheIleHisLeuLeuLeuGlnAaGgLyIle	354
Db	1020	ATACTGGTTGAAGCACTGTCTGCATTCAGAGGAACTCAAGCTGTCTCGAACAATCTCC	1079
QY	355	GlyIuHnIsGlnLyvThrGlnGlyLeuAaGAlaIleMetAaAsnAaGgGlnLeuLeuAsp	374
Db	1080	AATGAGCTGTATAGAAATTCAGAGCTTCCATCTCTGATAGAAATATCAACCACTGTATTGAC	1139
QY	375	GlnCySeGlnValProAlaValGlySerLeuIleCySeAlaIleuGlnLeuGlnAspVal	394
Db	1140	CAATGCCAGGCCCCCTGTGTGTGCTCCCTGTGTGTAGAGCTTACACTACAGAAAGAA	1199
QY	395	ValGlyGlnSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaIlePheVal	414
Db	1200	CTGGGAAAGAGATGACACCTTACCTCCGCAAGACTCTCACCGGTTTGTATGCCAGTTGGTG	1255
QY	415	PheHisGlnLeuThrProArgGlyValAlaArgArgCySeuAsnLeuGlnIuArgVal	434
Db	1260	TTTTCACCAAGCTCACCTTGAAAGAGCGTTCCAGAGCGCTTCAGTCAGAAAGAACAGATT	1311
QY	435	ValLeuLyAspArgPheCySeArgMetAlaValGlnGlyValITTPAsnAaGlySerValPhe	454
Db	1320	ACTCTAGCGGGTTTGTGATGATGAGCAAGCTAAGAGAGTGAGCAATGAGGCTGGTGTTC	1377
QY	455	AspGlyAspAspLeuMetValGlnGlyLeuGlyGlnSerGlnLeuAaGAlaLeuPheHis	474
Db	1380	TATGATGATGAACTCGAAGAACTATAGCTTAAGAGAGCTTGAGATTTGGCCTCTTTGAC	1433
QY	475	MetAsnIleLeuLeuProAspSerHis--CySeGlnIuArgLyThrPhePheHisIleu	493
Db	1440	ATGAAACATCTTCTCCAGGTGGCCACAACAAGTAGAGAGTGTTAGTTTCTCCACCTC	1499
QY	494	SerLeuGlnAspPheCySeAlaIleuLyThrValIleuGlnGlyLeu--GlnIleGln	512
Db	1500	AGCTGCGAGATTTCTTGTGCTGCTTATATATGTTTAAAGGCGCTGAGAGAAAGCAAT	1553
QY	513	ProAlaLeuCySeProLeuLyThrValGlnLySerThrLyAspSerMetGlnLeuLyGlnIle	532
Db	1560	CAGCATTTTTC-----TTTCATTTGAAACCAAGAACATCATGAGAGTGAAGAAACT	1611
QY	533	GlyPheHisIleHisSerLeuThrPheLyAspArgPheLeuPheGlyLeuValSerGlnAsp	552
Db	1614	GAC--GACACTCGGCTCTCGGAGTGAAGCTTTCTTATTTGGCTCATGAACAAGAT	1670
QY	553	ValArgArgProLeuGlnValIleuLeuGlyCySeProValProLeuGlyValIleGlnLyAs	572
Db	1671	ATCTTGAAAGACTCGAGAGTTCTGTGTTGAATATCCGATGATTCACATGTTAGACAGAAG	1730
QY	573	LeuLeuHisITrPValSerLeuLeuGlyGlnGlnProAsnAlaIThrThnProGlyAspThr	592
Db	1721	CTCCAACTGGGTCTCTGTATACCTCAGCAGGCTCAATGGCACCAAGCCCAATGACACC	1791
QY	593	LeuAspAlaPheHisCySeLeuPheGlnThrGlnAspLyGlnPheValArgLeuAlaLeu	612
Db	1791	CTGATGCTTCTTATTTGCTATTTAGCTCTCAGAGTGAAGATTTGTTGGCGGGCTCTC	1855
QY	613	AsnSerPheGlnIuValITrPLeuProIleAsnGlnAsnLeuAspLeuIleAsSerSer	632
Db	1851	AAAGCTTCCAAGAGATGGGTGCTGTGATTAACAGAAAGATGACCTTGAGGCTCTTCTCC	1911
QY	633	PheCySeLeuGlnHisCySeProTyLeuArgLyIleArgValAspValIleSerIlePhe	652
Db	1911	TACTCTTCCAAGACTGTCAAGAACTTGAAGCAATCCGGGTGAGATATACAGAACTCTCTC	1977
QY	653	ProArgAspGlnSerAlaGlnAlaCySeProValValProLeuITrP--MetArgAspLyAs	671
Db	1971	TCCGTAGATTAATCTCTGAGCTGGTCCCTGTGTTTACTGTCTCAGAGACACAAATGTAA	2033
QY	672	ThrLeuIleGlnGlnITrPGLyAspPheCySeSerMetLeuGlyThnHisITrPLeu	691
Db	2031	CCCTCTCTCAATGAGATGGTGGGAAACTTTGCTGTGTGCTTGGCAGCCTCCGAAACTTG	2099
QY	692	ArgGlnLeuAspLeuGlySerSerIleLeuThrGlnAaGAlaMetLyThrLeuCySeAla	711

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Db      2091 AAGAGCTGACCTGGGCGACAGCATCTCGATCAAGGCGCAATGATATCTGCTC 2150
      712 LysLeuArgHisProThrCysLysIleGlnThrLeuMetPheArgAlaGlnIleThr 731
      2151 GACCTGGGAGATCACTCTCCAGAAATCAAGAACTGACGTTTAAAGATGACAGAGTGTG 2210
      732 ProGlyValGlnHisLeuThrPargIleValMetAlaAsnArgAlaGlySerLeuAsn 751
      2211 TCTGGCTGAAACCTCTCTGGAAGCTCTTTTAAAGATCAAAACCTTAAAGTACCTCAAT 2270
      752 LeuGlyGlyThrHisLeuLysGluValAspValArgMetAlaCysGluAlaLeuLysHis 771
      2271 CTAGGGAACAACCTCCCATGAAGATGATGATGAAGTTAGCTGCGAAGCGCTGAACAT 2330
      772 ProLysCysLeuLeuGlnSerLeuArgLeuAspCysGlyLeuThrHisAlaCysTyr 791
      2331 CCAAGTGTCTCCGAGGAGCTGTGAGGCTGTGATTCCTGTAGATTAAACCATCATTTGTTAT 2390
      792 LeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuAlaGly 811
      2391 GAAGATGATCTCCACGCTTCTTATTTCACACCAAGCTTAAAGTCTCAAGCTGGCCAAA 2450
      812 AsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCys 831
      2451 AATAGAGTGGAGATAAAGAGATGATATCCCTTGGAAATGCTTGAAGTACTCAATGTGT 2510
      832 AlaLeuGlnLysLeuIleLeuGlnLysAspCysGlyLysLeuThrHisGlySerGlnSerLeu 851
      2511 CTACTGAAAGATTGATATCTGGAACATGTCGCTGACCTGACCTGACCTGACCTTCTGT 2570
      852 AlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLysSerAsnSerLeu 871
      2571 GTCTCAGCCCTTTTCAAGCAACCAACTTGAACAACCTGTGCTGTCAACCAAGCTGTG 2630
      872 GlyAsnGlnGlyValLeuLeuLeuCysArgSerMetArgLeuProHisCysSerLeuGln 891
      2631 GGGAGTGAAGAGTGAACAGCTGTGTCAAGTTCCTGAAGAAATCCAGATGTGCTCCAG 2690
      892 ArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAla 911
      2691 CGGCTGATGACTGATCACTGCAACATTTGATGATGATGCTTAAAGCTTCTGCGCAATAGA 2750
      912 LeuMetGlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsn 931
      2751 CTTGCAACAACAACAAGCTGACCCCACTGAGCTGACATGAACCCCGTAGGGAGTGT 2810
      932 GlyValLysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGlu 951
      2811 GCATGAGAGTACTGTGTGAAGCTTTAAAGAACCTTACTTGTACCTTCAAGAACTGGAA 2870
      952 LeuValLysCysHisLeuThrAlaAlaCysGlySerLeuSerCysValIleSerArg 971
      2871 CTATGTGACCTGCCAATCTCACACAGAACTGTGCGAGGACCTGGCTGTATATCAACAACA 2930
      972 SerArgHisLeuLysSerLeuAspLeuThrAspAlaLeuGlyAspGlyGlyValAla 991
      2931 ACCAAGCACTTAAAGTTTGGATCTTGTAACAAGCCCTGGGTGACAAAGAGTCAATA 2990
      992 AlaLeuCysGlnGlyLeuLysGlnLysAsnSerValLeuThrArgLeuGlyLeuLysAla 1011
      2991 ACCCTGTGTAGGAGTGAAGCAAAAGTACAGCTCCCTGAGAGAGACTTGGGGGCA 3050
      1012 CysGlyLeuThrSerAspCysGlyValAlaLeuSerLeuAlaLeuSerCysAsnArgHis 1031
      3051 TGTATGATGACTTCCCAATGTCTGTAGAGCAATGTGATGGCCATCTTGTGAACCTCTCAC 3110
      1032 LeuThrSerLeuAsnLeuValGlnAsnAspHisSerProLysGlyMetMetLysLeuCys 1051
      3111 CTGAACAGCTTAAACCTGTGTGAAGATGATCTTCAATGATCGGGGATGTTGAAGCTGTGC 3170
      1052 SerAlaPheAlaCysProThrSerAsnLeuGlnIleLeuGlyLeuTrpLysTrpGlnTyr 1071

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Db      3171 TCTGCGTTCCAAATCCCTGTCTCTAACTGGGAGTAAATTTGGCCTGTGGAACGAGAGTAC 3230
      1072 ProValGlnIleArgLysLeuLeuGlnValGlnLeuLeuLysProArgValAlaIle 1091
      3231 TAGCCCGAGATGAGAAAGACAGCTGTGAGGAAGTTGAGTTTGTCAAGCCCAAGTGTGATT 3290
      1092 AspGlySerTrpHisSerPheAspGluAspAspArgHis 1104
      3291 GATGTGATTTGTATGTACTAGTATGAAGATGACCGAACAAC 3329

RESULT 12
US-10-399-443-1
/ Sequence 1, Application US/10399443
/ Publication No. US20040028669A1
/ GENERAL INFORMATION:
/ APPLICANT: The Government of the United States of America, as Represented by the
/ APPLICANT: Secretary, Department of Health & Human Services, The National Institute
/ APPLICANT: Health
/ APPLICANT: Nelson, Lawrence M.
/ APPLICANT: Tong, Zhi-Bin
/ APPLICANT: Nelson, Lawrence
/ APPLICANT: Zhi-Bin, Tong
/ TITLE OR INVENTION: Human Gene Critical to Fertility
/ FILE REFERENCE: 4239-64785
/ CURRENT APPLICATION NUMBER: US/10/399,443
/ CURRENT FILING DATE: 2003-04-16
/ PRIOR APPLICATION NUMBER: 60/241,510
/ PRIOR FILING DATE: 2000-10-18
/ PRIOR APPLICATION NUMBER: PCT/US01/10981
/ PRIOR FILING DATE: 2001-04-04
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 1157
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-399-443-1

Alignment Scores:
Pred. No.: 2,536-203 Length: 1157
Score: 2005.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.34% Indels: 0
DB: 7 Gaps: 0

US-10-066-521-6 (1-1344) x US-10-399-443-1 (1-1157)
      252 GlnAlaProValThrGlnIleMetSerArgProGlnArgLeuLeuPheIleIleAspGly 271
      1 CAAGCTCCGGTGAACGAGATCATGTCCCGACCAAGAAAGCTGTGTTCATCATTTGACGGGT 60
      272 PheAspAspLeuGlySerValIleuAsnAspThrLysLeuCysLysAspTrpAlaGlu 291
      61 TTCATGACCTGGGCTGTGTCTTCAACAATGACCAAAAGCTCTGCAAAAGACTGGGCTGAG 120
      292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
      121 AAGCAGCCTCCGTTCAACCTCATACGACAGTCTGTGAGGAAGTCCGCTGCTCCGAGTCC 180
      312 PheLeuIleValThrValArgAspValGlyThrGlnLysLeuLysSerGlnValValSer 331
      181 TTCCTGATCGTCAACCGTCAAGAGAGTGGGCAAGAGAACTCAAGTCAAGAGTGTGTCT 240
      332 ProArgTrpLeuLeuValArgGlyLysSerGlyGlnGlnArgLysIleHisLeuLeuGlu 351
      241 CCCGTTACCTGTATGTTAGGAGATCTCCGGGGAACAAAGAACTCTGCTCTTGAG 300
      352 ArgGlyIleLeuGlnHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAspArgGlu 371
      301 CGCGGATGTGTGTGACATCAAGAACACAAAGGTTGTGCTGCATCAAGAACACCTGTGAG 360
      372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391

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Db 361 CTGCTGACCAAGCTCCAGGCTCCGCGGCTCTCATCTGCGGCTCCAGCTG 420
Qy 392 GlnAapValVal1GlyGluSerVal1AlaProPheAenGlnThrLeuThrGlyLeuHisAla 411
Db 421 CAGGACGTGGTGGGGAGAGCGTGGCCCTTCAACCAAGCTCCAGGCTCCAGCC 480
Qy 412 AlaPheValPheHisGlnLeuThrProArgGlyVal1AlaArgArgCysLeuAenLeuGln 431
Db 481 GCTTTGTTGTTCAATGAGCTCAACCTGAGCGGCGGCTCCGCTCATATCTGGAG 540
Qy 432 GlnArgVal1Val1LeuLeuArgPheCysArgMetAlaVal1GluGlyVal1TrpAsnArgLys 451
Db 541 GAAAGAGTTGCTCCGAAGCGCTTCTGCGGTATGCTGCGAGGAGGTGTGAATAAGAG 600
Qy 452 SerValPheArgGlyAspAspLeuMetVal1GlnGlyLeuGlyGluSerGlyLeuArgAla 471
Db 601 TCAGTGTTCAGCGGTGAGACCTCATGTTCAAGGACTCGGGGAGTCTGAGCTCCGTCT 660
Qy 472 LeuPheHisMetAsn1LeuLeuProArgSerHisGlyGluGlyTrpThrPhePhe 491
Db 661 CTGTTTCAATGAAATCTCTTCTCCAGACAGCCACTGAGAGTACTACACTTCTTC 720
Qy 492 HisLeuSerLeuGlnAspPheCysAla1AlaLeuTrpVal1LeuGluGlyLeuGluLe 511
Db 721 CACCTCAGTCTCCAGAGCTTCTGTCGCCCTTGTACTACGTCTTAGAGGCGCTGGAATC 780
Qy 512 GlnProAlaLeuCyProLeuTrpVal1GlyThryThryArgSerMetGlyLeuLysGln 531
Db 781 GAGCAGCTCTCTGCGCTCTGTATGAGAAAGAAAGAGTCCATGAGCTTAAACAG 840
Qy 532 AlaGlyPheHisGlyLeuSerLeuTrpMetLysArgPheLeuPheGlyLeuValSerGlu 551
Db 841 GCAGGCTTCATATCTCCTGCTTGTGATGAAAGCGTTCTGTGTGCGCTGAGGCA 900
Qy 552 AspVal1ArgArgProLeuGlnVal1LeuLeuGlyCysProVal1ProLeuGlyVal1LysGln 571
Db 901 GACGTAGAGAGGCGCACTGAGAGTCTGCTGCGCTGTCCGTTCCCTGGGGTGAAGCAG 960
Qy 572 LysLeuLeuHisGlyTrpVal1SerLeuLeuGlyGlnGlnProAsnAla1ThrThrProGlyAsp 591
Db 961 AAGCTTTCAGACTGGGTCTCTCTGTGTGGTCAAGAGCTTAAATGCCACCAAGCTTGAAGCAG 1020
Qy 592 ThrLeuAspAlaPheHisCysLeuPheGlnThrArg1AspLysGlnPheVal1ArgLeuAla 611
Db 1021 ACCCTGAGCGGCTTCAGTCTTTCATGAGACTCAAGCAAGAGTTGTGCTTGCA 1080
Qy 612 LeuAsnSerPheGlnGlnVal1TrpLeuPro1LeuGlnAsnLeuAspLeu1LeuAsnSer 631
Db 1081 TTAAACAGCTTCAGAAAGTGGCTTCGATTAACAGAACTGGAATTGATACATCT 1140
Qy 632 SerPheCysLeuGln 636
Db 1141 TCCTTCTGCTCCAG 1155

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; PRIOR APPLICATION NUMBER: PCT/US01/10981
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-677-943-1

Alignment Scores:
Pred. No.: 2,536-203 Length: 1157
Score: 2005.00 Matches: 385
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 28.34% Indels: 0
DB: Gaps: 0

US-10-066-521-6 (1-1344) x US-10-677-943-1 (1-1157)
Qy 252 GlnAapProVal1ThrGlu1LeuMetSerArgProGluArgLeuPhe1LeuAspGly 271
Db 1 CAGGCTCCGTTGACGGAGATCATGTCCGACCAAGAGCGTGTGTTTATCATATGACGCT 60
Qy 272 PheAspAspLeuGlySerVal1LeuAsnAsnAspThryThryLysCysLysAspTrpAlaGlu 291
Db 61 TTCATATGACTGGGCTGTCTCTCATACATGACAAAGCTCTGCAAGAGCTGGGCTGAG 120
Qy 292 LysGlnProProPheThrLeu1LeuArgSerLeuLeuArgLysVal1LeuLeuProGlySer 311
Db 121 AAGCAGCTCCGTTCACTCATACGAGTCTGCTGAGAAAGTCTGCTCCAGATCC 180
Qy 312 PheLeu1LeuVal1ThrVal1ArgAspVal1GlyThrGluLysLeuLysSerGluVal1Ser 331
Db 181 TTCGATGTCACCGTACAGAGAGTGGGCAAGAGAGCTCAAGTCAAGAGCTGTCT 240
Qy 332 ProArgTrpLeuLeuVal1ArgGly1LeuSerGlyGlnArg1LeuHisLeuLeuGln 351
Db 241 CCCGTTTACCTGTTATGTTAAGGAATCTCCGGGGAACAAAGATCACTTGCCTCTGAG 300
Qy 352 ArgGly1LeuGlyLysGlnGlyThryThryGlnGlyLeuArgAla1LeuMetAsnAsnArgGlu 371
Db 301 CGCGGATTTGTTGATCAGACAGAAAGCAAGAGTGTCTGCGATCATTAACAACCGTAG 360
Qy 372 LeuLeuAspGlnCysGlnVal1ProAlaVal1GlySerLeu1LeuCysVal1AlaLeuGlnLeu 391
Db 361 CTGCTGACCAAGTCCAGGTCGCCGCGGTCTCTCATCTGCGGCTCCAGCTG 420
Qy 392 GlnAapVal1Val1GlyGluSerVal1AlaProPheAenGlnThrLeuThrGlyLeuHisAla 411
Db 421 CAGGACGTGGTGGGGAGAGCGTGGCCCTTCAACCAAGCTCCAGGCTCCAGCC 480
Qy 412 AlaPheVal1PheHisGlnLeuThrProArgGlyVal1AlaArgArgCysLeuAenLeuGln 431
Db 481 GCTTTGTTGTTCAATGAGCTCAACCTGAGCGGCGGCTCCGCTCATATCTGGAG 540
Qy 432 GlnArgVal1Val1LeuLeuArgPheCysArgMetAlaVal1GluGlyVal1TrpAsnArgLys 451
Db 541 GAAAGAGTTGCTCCGAAGCGCTTCTGCGGTATGCTGCGAGGAGGTGTGAATAAGAG 600
Qy 452 SerValPheArgGlyAspAspLeuMetVal1GlnGlyLeuGlyGluSerGlyLeuArgAla 471
Db 601 TCAGTGTTCAGCGGTGAGACCTCATGTTCAAGGACTCGGGGAGTCTGAGCTCCGTCT 660
Qy 472 LeuPheHisMetAsn1LeuLeuProArgSerHisGlyGluGlyTrpThrPhePhe 491
Db 661 CTGTTTCAATGAAATCTCTTCTCCAGACAGCCACTGAGAGTACTACACTTCTTC 720
Qy 492 HisLeuSerLeuGlnAspPheCysAla1AlaLeuTrpVal1LeuGluGlyLeuGluLe 511
Db 721 CACCTCAGTCTCCAGAGCTTCTGTCGCCCTTGTACTACGTCTTAGAGGCGCTGGAATC 780
Qy 512 GlnProAlaLeuCyProLeuTrpVal1GlyThryThryArgSerMetGlyLeuLysGln 531

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RESULT 13
US-10-677-943-1
; Sequence 1, Application US/10677943
; Publication No. US20040072297A1
GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; REPRESENTED by the Secretary of the Department of Health and
; HUMAN SERVICES
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29

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Db      781  GAGCGAGCTCTGCCCTCTGTAGTTGAGAGACAAAGAGTCCATGAGCTTAACAG 840
Qy      532  AAGlyPhehi81lehi8serleuTPMeLyArpPheleuPhegiyleValSerGlu 551
Db      841  GCGAGCTTCATATCCACTGCTTGGATGATGAGGTTCTTGTGGCTGGAGGAA 900
Qy      552  AspValArgArpProleuGluValleuLeuGlyCySerProValProleuGlyValLyGln 571
Db      901  GAGCTAAGAGGCGCACTGAGAGTCTCTGGCTGCTCCCTCCCTCCGGGGGTGAACAG 960
Qy      572  LyLeuLeuHi81rTPValSerleuLeuGlyGlnInPro8analrThrProGlyASP 591
Db      961  AAGCTTCGACGTGGTCTCTGTGGTCAAGAGGCTAATGCAACCCCGAGAGAC 1020
Qy      592  ThrleuAspAlaPhehi8CySerleuPheGluThrGlnAspLySerGluPheValArgLeuAla 611
Db      1021  ACCCTGAGCGCTTCCACTGTCTTTCGAGACTCAAGACAAAGATTGTTCGCTTGGCA 1080
Qy      612  LeuAspSerPheGlnGluValITrPLeuProIle8nGlnAsnLeuAspLeuIleAlaSer 631
Db      1081  TTAAACAGCTTCCAAAGAGTGGCTTCCATTAACAGAACTGAGCTTGAATAGCATCT 1140
Qy      632  SerPheCySerleuGln 636
Db      1141  TCCTTCTGCTCCAG 1155

RESULT 14
US-10-794-342-2
; Sequence 2, Application US/10794342
; Publication No. US20040253615A1
; GENERAL INFORMATION:
; APPLICANT: Inohara, Naohiro
; APPLICANT: Nunez, Gabriel
; TITLE OF INVENTION: NOD Nucleic Acids and Polypeptides
; FILE REFERENCE: UM-08922
; CURRENT APPLICATION NUMBER: US/10/794,342
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-794-342-2

Alignment Scores:
Pred. No.:          9,56e-190      Length:      3521
Score:              1885.50        Matches:      422
Percent Similarity: 56.65%         Conservative: 208
Best Local Similarity: 37.95%      Mismatches:   443
Query Match:        26.65%         Indels:       39
DB:                 8              Gaps:         13

US-10-066-521-6 (1-1344) x US-10-794-342-2 (1-3521)
Qy      2  GlnGlyAspLySerleuThrPheSerSerTyGlyLeuGlnTrpCyLeuTyGluLeu 21
Db      28  GATTCATCATCATCTTCTTCTTCCGATTTTGGGCTGCTATGTATTTGGAGAGACTA 87
Qy      22  AspLySerGlnGluPheGlnThrPheLySerGluLeuLeuLySerSerSerGluSerThr 41
Db      88  AACAAAGAGAAATTAATATCACTCAAG---TTATTCCTAAAGAGAGCAATGAACTGAG 144
Qy      42  ThrCySerleuPheProGlnPheGlnIleGluAsnAlaAsnValGluCySerleuAlaLeu 61
Db      145  CATGGCTGACACCCCTGGAATGAAAGTGAAGAGCGGCGAGAGCACTGGCCAATTTG 204
Qy      62  LeuHi81GlyTyGlyAlaSerleuAlaTrpAlaThrSerleuSerleuPheGluAsn 81
Db      205  ATGAAAGAAATTTATTCAGAGAGAGAAAGCTCGAGTGTCTCTCAAAATCTTTGGCAG 264
Qy      82  MetAsnLeuArgThrLeuSerGluLyAlaArgAspMetClySerleuSerGlnAla 101
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Db      265  ATGAACTTGAGGATGTGTGTGAGAGAGCAAGAAAGAGATCAACTGTGCGCCAGACT 324
Qy      102  MetGlnGlnGluLyAlaThrAlaAlaGluThrGlnGlnGlnIleSerGlnAlaMet 121
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Qy      122  GlnGlnGlnGlyAlaThrAlaAlaGluThrGlnGlnGlnIleIleGlyIleAspThrTrp 141
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Qy      142  AspTyTrpSerHi8ValMetThrLyPheAlGlnGluAspValAlaArgSerPhe 161
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Qy      176  GlyAlaPheAspSerAsp--ArgTrpGlyPheArgProArgThrValValLeuHi8Gly 194
Db      511  CACTGTTCATGTGATGTATGTCAAACCGGTGCACAGCACAGATCGTGGCTTCAGGGA 570
Qy      195  LySerGlyTleGlyLySerAlaLeuAlaArgArgTleValLeuCySerTrpAlaGlnGly 214
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Qy      235  LyLeuSerGluSerValThrgluPheIleSerArgGluTrpProAspSerGlnAlaPro 254
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Qy      255  ValThrgluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAsp 274
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Qy      394  ValValGlyLeuSerValAlaProPheAsnGlnThrLeuThrglyLeuHi8AlaAlaPhe 413
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 Qy 474 HisMetAsnIleLeuLeuProAspSerHisCysGlnGlnGlyTyrTyrPhePheHisLeu 493  
 Db 1405 GACAGCATATTTATTCAGAGAGCCAGAGATATGAAACTGTATGTTTACCCACTT 1464  
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 Qy 551 GluAspValArgAspProLeuGlnValLeuLeuGlyCysProValProLeuGlyValIys 570  
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 Qy 611 AlaLeuAsnSerPheGlnGlnValIlePheLeuProIleAsnGlnAsnLeuAspLeuIleAla 630  
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 Qy 711 AlaLysLeuAspGlnProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIle 730  
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 ; Sequence 23, Application US/10124498  
 ; Publication No. US20030017983A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bertin, John  
 ; APPLICANT: Wang, Weiye  
 ; APPLICANT: Blatcher, Maria  
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR  
 ; FILE REFERENCE: 0734-367001  
 ; CURRENT APPLICATION NUMBER: US/10/124,498







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GenCore version 5.1.6  
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1434	20.3	2985	US-10-781-294-15	Sequence 15, Appl
2	1320.5	18.7	3108	US-10-781-294-23	Sequence 23, Appl
3	955	13.5	4287	US-09-996-617-5	Sequence 5, Appl
4	955	13.5	4422	US-09-388-221B-1	Sequence 1, Appl
5	955	13.5	5444	US-09-996-617-1	Sequence 1, Appl
6	949	13.4	4200	US-09-388-221B-3	Sequence 3, Appl
7	949	13.4	4332	US-09-388-221B-5	Sequence 5, Appl
8	948	13.4	4466	US-09-388-221B-11	Sequence 11, Appl
9	945.5	13.4	4556	US-09-388-221B-9	Sequence 9, Appl

10	911	12.9	4931	US-10-183-770A-1	Sequence 1, Appl
11	721	10.2	2844	US-10-781-294-17	Sequence 17, Appl
12	705	10.0	2524	US-10-781-294-58	Sequence 58, Appl
13	672.5	9.5	2068	US-10-104-047-63	Sequence 63, Appl
14	646	9.1	2046	US-10-781-294-19	Sequence 19, Appl
15	630.5	8.9	1374	US-08-910-731-3	Sequence 3, Appl
16	630.5	8.9	1374	US-08-795-395-3	Sequence 3, Appl
17	621	8.8	1371	US-08-910-731-1	Sequence 1, Appl
18	621	8.8	1371	US-08-795-395-1	Sequence 1, Appl
19	612	8.7	1371	US-08-910-731-7	Sequence 7, Appl
20	607.5	8.6	1386	US-08-910-731-5	Sequence 5, Appl
21	544.5	7.7	2689	US-10-028-347-1	Sequence 1, Appl
22	527	7.4	2763	US-10-028-347-5	Sequence 5, Appl
23	406	5.7	3156	US-09-799-451-870	Sequence 870, Appl
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32	364	5.1	3123	US-10-002-974-66	Sequence 66, Appl
33	364	5.1	3123	US-10-002-974-84	Sequence 84, Appl
34	364	5.1	4390	US-09-949-002-101	Sequence 101, Appl
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40	363	5.1	4384	US-09-949-002-238	Sequence 238, Appl
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42	362	5.1	3123	US-10-002-974-60	Sequence 60, Appl
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45	360	5.1	3123	US-10-002-974-88	Sequence 88, Appl

## ALIGNMENTS

RESULT 1  
US-10-781-294-15  
Sequence 15, Application US/10781294  
Patent No. 6953691  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Godzik, Adam  
APPLICANT: Chu, Zhi-Liang  
APPLICANT: Pawlowski, Krzysztof  
APPLICANT: Fiorentino, Ioredana  
APPLICANT: Ariana, Maria Bugenia  
APPLICANT: Stenlik, Christian  
TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,  
FILE REFERENCE: P-LJ 4816  
CURRENT APPLICATION NUMBER: US/10/781,294  
CURRENT FILING DATE: 2004-02-17  
PRIOR APPLICATION NUMBER: US/09/965,621  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: US 09/671,760  
PRIOR FILING DATE: 2000-09-26  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 2985  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(2985)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(1857)

OTHER INFORMATION: n = A, T, C or G  
US-10-781-294-15

Alignment Scores:	
Pred. No.:	4,57e-134
Score:	1434.00
Percent Similarity:	48.27%
Best Local Similarity:	3.04%
Query Match:	20.27%
DB:	3
	Gaps: 12
	Length: 2985
	Matches: 339
	Conservative: 199
	Mismatch: 430
	Indels: 124
	Gaps: 12

US-10-066-521-6 (1-1344) X US-10-781-294-15 (1-2985)

QY	9	PhesSerSerTgclYleuGIInPrCySleuYrgIleuAapYleuGIInPhGIIntr	28
Db	16	TTCTCTGATTTTGGTCTTATGTGTGATCTGGAGAGCTCAAAAAGAGAGATTCAGAAA	75
QY	29	PhelyGsluDeuLeuYlsYlsYsSerSerGIuSerThrThrCySerIleProGIInPhe	48
Db	76	TTTAAAGAACATCTCAAGCAAAATGACTTTGGACGTTGAATCAAGCAAGATTCCTGGACT	135
QY	49	GIuIIeGIuBsmAlaSnValGluCyBleuAlaLeuLeuLeuHleGIuYrTyGlyAla	68
Db	136	GAGGTCAAAAAGCAATCCCGGAGAAAGAACTTGAAACCTTGATCAAGCACTTAAAGAA	195
QY	69	SerLeuAlaTrpAlaThrSerIleSerIlePheGIuAmeAmeLeuAArgThrLeuSer	88
Db	196	CAACAAAGCTTGAACATTAACCTTAAAGATCTTCAAAAGATG-----	237
QY	89	GIuIyAlaArgAapMecIySylIeSerGIuAlaMetGIuGIInGIuAlaThr	108
Db	238	-----GATAGAAAGAGATCTCTCATAGAGAGATCATAGAGAGAGAAACAGA	288
QY	109	AlaAlaGIuThrGIuGIInGIuIleSerGIuAlaMetGIuGIInGIuAlaThrAla	128
Db	283	TACACAAAGCTTATCAAGCTCAGCGAAAGCAAAATTCAGCCGC-----	327
QY	129	AlaGIuThrGIuGIInGIuIleGIyAlaSerThrTrpApyrTyIySerHleValMet	148
Db	328	-----TTATGGTCCAGCAAGTGTGTACAGAG	354
QY	149	ThrIySerPheAlaGIuGIuIleApyrAlaArgAArgSerPheGIuAmeThrAlaAlaPTrp	168
Db	355	ATTCAACCTATCTTGAAGAGAAAGTCAAGAA-----	390
QY	169	ProGIuMetGIInThrIleuAlaGIyAlaPheAapSerApyrTgYlPheArgProArg	188
Db	391	---GAATGTGACCATTTTGGACCGCTTTTGTCTCCAGAAACGTGGAAACAGCAAGT	447
QY	189	ThrValIleuHleGIyIySerGIyIleGIyIySerAlaLeuAlaArgAlaIleVal	208
Db	448	ACAGTGTATTTATCAAGACCAACAGAAATTTGAAAAAGCACTCTGTATTAACATGATG	507
QY	209	IeuCySerPheAlaGIInGIyIleuYrGIInGIyMetPheSerYrValPhePheLeuPro	228
Db	508	ATGCGCTGGTGGAGCAACAAGATCTTTGGATAGGTCCTGTACACGTTATATTCTGC	567
QY	229	ValArgGIuMetGIInArgIyIySgiuSerSerValThrGIuPheIleSerArgIuTrp	248
Db	568	TGCAGAGAACTGAGGGAGTTGCCGCAACGATTTGGCTGACTGATTTCCAGAGATGG	627
QY	249	ProAapSerGIInAlaProValThrGIuIleMetSerArgProGIuArgLeuLeuPheIle	268
Db	628	CTGAGCCCCGCTCTCTTAACACAGAGATCGGTCTCAACCGAGAAAGCTTTTGGTC	687
QY	269	IleAapGIyPheAapAapLeuGIySerValIleuAmeAme---AapThrIleuCySyls	287
Db	688	ATGACAGCGTTGCAAGAGGTGACGAGCGGCTTGAAACGAACCGAATTCGATCTGTGGT	747
QY	288	AapTrpAlaGIuIySgiuProProPheThrIleuIleArgSerLeuLeuArgIyValLeu	307
Db	748	GACTTGAATGAGAAACGGCCGGTGACAGTGTCTTGACAGATTTGGCTGAGAAAGATG	807

QY	308	LeuProGluSerPheLeuIleValThrValArgAspValIGlyThrGluLeuValSer	327
DB	808	CTCCGGAGGGCTCCCTCTATGCCATCAAAACCCGTGTGCCAAGAGCTCCGGAT	867
QY	328	GluValValSerProArgTyrIleuDeuValArgGlyIleSerGlyGluIlnArgIleHis	347
DB	868	CAGGTGAAGATCTCAGAATCTACACAGCCCGGGAGATTCAACGAGATGATAGTTAAG	927
QY	348	LeuIleuLeuGluArgGlyIleGlyIleuIleGlnIleGlnIleuArgAlaIleMet	367
DB	928	TATTTCTGCTGTTCTTCAAAAGCCCGAAAGAGCCATGAAAGCTTCAATCTGTAA	987
QY	368	AsnAsnArgGluLeuLeuAspGlnCySerGlnValProAlaValGlySerLeuIleCyVal	387
DB	988	GAAAGTGAACAGCTGTTTTCCATATGCAAAATCCGCTCTCTGTGGATCCGTGTACC	104
QY	388	AlaLeuGlnLeuGlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThr	407
DB	1048	AGCTGAAGCAAGAGATCCAGAAAGGAAAGAAAGCTTGGCTGACCTGCCAGAGCACTAC	110
QY	408	GlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCy	427
DB	1108	TCTGTGATCTCTCTTGTCTTTAACTGTTTCAACCTTGAAGGTTGCCAAGGCCCACT	116
QY	428	LeuAsnLeuGluArgValArgValValLeuValArgPheCyArgMetAlaValGluGlyAl	447
DB	1168	CCGCAAAACCCAGACACAG-----CTGAAGGCCCTGTGCTCTGCTGCTGACAGAGGTATG	122
QY	448	TrpAsnArgIleSerValPheAspGlyAspArgLeuMetValGlnGlyLeuGluSer	467
DB	1222	TGGACAGACACATTTGAAGTTTGTGAACACACTCCCGAGAAATGGGGTGTTCAGCGCT	128
QY	468	GluLeuAlaGAlaLeuPheHisMetAsnIleLeuLeuProAspSerHisCySerGluGluTyr	487
DB	1282	GACATCCCTGGCTGCTGTGGACCAAGATATCTTCTGAAGTACGGGAGCGTGAAGCTCC	134
QY	488	TyrThrPhePheHisIleLeuSerIleuGlnAspPheCyValAlaLeuTyrTyrValLeuGlu	507
DB	1342	TACGTGTCTCCCAAGTGTGATCCAGAGAGTTCTGTGCCCTGTGTCTAATTGTCTCAAG	140
QY	508	GlyLeuGluIleGluPro-----AlaLeuCySerProLeuTyr	519
DB	1402	AGCCATCTTGATCATCTCCACCCAGCTGTGAGATGTGAACAGATCTGTAATGCCAT	146
QY	520	ValGluIleThrIleAspArgSerMetGluLeuValGlnAlaGlyPheHisIleHisSerLeu	539
DB	1462	TTTGGAAAAGCAGGAGAGACA-----CATTGAGATT	149
QY	540	TrpMetIleAspPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluVal	559
DB	1492	TTTTTGGGGTGTTTCTAAGCTGGCTTTTAAATTAATAAAGAACAAAGAAAACTGGATGGC	155
QY	560	LeuLeuGlyCySerProValProLeuGlyValValGlyGlnIleIleThrValSerLeu	579
DB	1552	TTTTTTGGCTTCCAACTGCTCCCAAGATTAAGACGAAATTCACCAAGTGCCTGAAGAC	161
QY	580	LeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCyValLeu	599
DB	1612	TTAGGGGAGCGTGGCAATCTCAGGGACAGGTGATTCCTTGGCATATTTTAACGTCTC	167
QY	600	PheGluThrGlnAspIleGluPheValArgLeuAlaLeuAsnSerPheGlnGluValTrp	619
DB	1672	TTTGAATATGCAGATCTGCTCTTGTGAAGCAGGACGTGAACCTCTCCAAAGACTAAC	173
QY	620	LeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCyValLeuGlnHisCySerPro	639
DB	1732	TTTCAATATTAATGCAACGTGGAATTGGTGGTTTCTGCTACTGCTTTAAATACTGCTCC	179
QY	640	TyrLeuAspGlyIleArgValAspValValGlyIlePheProArgAspGluSerAlaGlu	659
DB	1792	AGCTTGAGAAACTGTGTTTTTCCGTCAAAATGCTTTAAGAAAGGATGAACACAGC	185
QY	660	AlaCySerProValValProLeuThrPheArgAspIleValIleGluGluGlnThrGlu	679

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Db      1852 TCT-----ACGCGGATTTACAGCTTCATC-----TGTTGGCAT 1884
Qy      AspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySerSer 699
Db      1885 CACATCTGCTCTGGAGCTCACACCGGAGCACTTCAGAGAGCTTCAGAGAGCAAGC 1944
Qy      700 IleuThrGlnValGlnMetLeuThrLeuCysValAluValMetArgHisProThrCysVal 719
Db      1945 ACCCTCAGCGAGCTGACCTTTGTGACCTGTGTAAACAGCTGAGGACATCCCAAGCTGTGCG 2004
Qy      720 IleGlnThrLeuMetPheArgAsnAlaGlnIleLeuProGlnValGlnHisLeuThrArg 739
Db      2005 CTTCAGAGAGCTTGGAAATTAATACCTTTCTTTCTGCGCCAGAGCTTCCTGCTTTAG 2064
Qy      740 IleValMetAlaAsnArgAsnLeuArgSerLeuLeuGlnGlyThrHisLeuValGln 759
Db      2065 GTGCTCTTTTATCAGCCAGACTTGGAAATACCTGAGCTTCACCTCAGCAAACTCTCTGCT 2124
Qy      760 GluAspValArgMetAlaCysGlnAlaLeuValHisProValCysValLeuGlnSerLeu 779
Db      2125 GATGACATCAGAGCTCCCTCTGTGATGCTTGAATCAACCA----- 2163
Qy      780 ArgLeuAspCysGlyLeuThrHisAlaCysTyrLeuValIleSerGlnIleLeuThr 799
Db      2163 ----- 2163
Qy      800 ThrSerProSerLeuValSerLeuSerLeuAlaGlnValMetValThrAspGlnVal 819
Db      2164 -----GCAGGCAAC----- 2172
Qy      820 MetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnValLeuGlnIle 839
Db      2173 -----GTCAAAAGACTAGCGGTGTA 2193
Qy      840 AspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsnArg 859
Db      2194 AATTGTCACTCTCACCACCATGATGTGTGAAGCTTGTGCGCTTCAACCAACAAG 2253
Qy      860 SerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlnValAsnGlnValAsnLeu 879
Db      2254 AAGCTGACGTATCTGAATGTATCTCGCAACCAAGTAA-----GACACAGCGCGCTTTTGG 2310
Qy      880 CysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCysHis 899
Db      2311 TGTGAAGCTCTGTGAGCCCAAGACAGCGCTCTGTATACCTGATGTGCTTTCTGCGCAC 2370
Qy      900 LeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeuThr 919
Db      2371 CTCAGCGAGCACTGCTGGGAATACATCTCTGAAAATGCTTTCGCTGACAGAGCGTGGCC 2430
Qy      920 HisLeuSerLeuSerMetAsnProValGlnAspAsnGlnValValLeuLeuCysGlnVal 939
Db      2431 TATCTAGACCTCAGTGCATATGCTCTGAAGAGCAAGAGCTGAAAATCTCTGCGAGGCGC 2490
Qy      940 MetArgGlnProSerCysHisLeuGlnAspLeuGlnValValCysHisLeuThrAla 959
Db      2491 TTGAACAATCCGAGACTGCTGTGATTCACCTGTGTGTAATAATGTTTATACACTGCT 2550
Qy      960 AlaCysCysGlnSerLeuSerCysValIleSerArgSerArgHisLeuValSerLeuAsp 979
Db      2551 GCTGCTGTGAAGACTGCGCTCTGCTCTCATCAGCAATCAAAACCTGAGAAATTTCTGCA 2610
Qy      980 LeuThrAspAsnAlaLeuGlnValAspGlyValAlaAlaLeuCysGlnGlyLeuValGln 999
Db      2611 ATTGGGTCAATGAATGAGATGATGGGTGAGAGCTGTGTGTGCGGCTCTGAGCAT 2670
Qy      1000 LysAsnSerValLeuThrArgLeuGlnValMetValAlaCysGlyLeuThrSerAspCys 1019
Db      2671 ACGGATTCGCGCTTGAGATTTTGTGGTTGGAAGAAATGTGGTTAAACGAGCACTGCTGT 2730
Qy      1020 GluAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSerLeuAsnLeuValGln 1039

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Db      2731 AAGGATTCGCGCTGTGTTCTCAGCTGAGTAAGACCTTCAGAGACTCAACCTGAGCTTG 2790
Qy      1040 AsnAsnPheSerProValGlyMetMetLeuValCysSerAlaPheAlaCysProThrSer 1059
Db      2791 AACACCTTGAACCAACAGAGGAGTGTGTATCTGTGAGGCTTCGAGACACCCAGAGTGT 2850
Qy      1060 AsnLeuGlnIleIleGlyLeuThrTrpGlnIleProValGlnIleArgValLeuLeu 1079
Db      2851 GCCCTGACAGTGTCTCGGCTGAGAAAACATGATTTGATGAGAAACCCAGAGCACTTCTG 2910
Qy      1080 GluGlnValGlnLeuLeuValProArgValAlaIle 1091
Db      2911 ACGGCTGAGAAAGAGAAATCTTAACCTGACCATC 2946

RESULT 2
US-10-781-294-23
; Sequence 23, Application US/10781294
; Patent No. 6953691
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAD Domain-Containing Polypeptides.
; TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/10/781,294
; PRIOR FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/965,621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3105)
US-10-781-294-23

Alignment Scores:
Pred. No.: 1.53e-122 Length: 3108
Score: 1320.50 Matches: 348
Percent Similarity: 47.33% Conservative: 175
Best Local Similarity: 31.49% Mismatches: 455
Query Match: 18.67% Indels: 127
Dels: 3 Gaps: 19

US-10-066-521-6 (1-1344) x US-10-781-294-23 (1-3108)
Qy      18 LeuTyrGlnLeuAspArgGlnGluPheGlnThrPheValGlnLeuValValSerSer 37
Db      49 TTGAAGAACTCGAGAGCTGTGACTGTAAGAACTCAAG---TTATACCTGGGAGCGCG 105
Qy      38 SerGlnSerThrThrCysSerIleProGlnPheGlnIleGlnValAsnAlaAsnValGlnCys 57
Db      106 ACAAGAGCTGGAGAAAGCAAGATCCCTCGGGAGAGCATGAGAAAGCGCGTCCCTGGAA 165
Qy      58 LeuAlaLeuLeuLeuHisGlnTyrGlyAlaSerLeuAlaTrpAlaThrSerIleSer 77
Db      166 ATGGCCAGCTGCTCATGACCACTTCGGGCCAGAGAGGCGCTGAGGTTGGCTCTCAGC 225
Qy      78 IlePheGlnAsnMetAsnLeuArgThrLeuSerGlnValAla----- 91
Db      226 ACCTTTGAAGCGGATTAACAAGAAAGCACTGTGGGAGAGAGACAGAGAGAGCACTGGTG 285
Qy      92 -----ArgAspAspMetLeuValValIleSerGlnAlaMetGln 104

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Db      286 AGGATGCCAGAAACCTACAGGACTATGTCGCGAGAAATTCGGCTCATGGAAGAC 345
Qy      105 GluGluValThrAlaAlaGlu-----ThrGluGluGluGluIleSerGlnAlaMet 121
Db      346 CGCAATGCGCGCTAGGGGAATGTGTCAACCTCAGCCACCGGCTCTGCTGCTG 405
Qy      122 GluGluGluGluValThrAlaAlaGluThrGluGluGlu-----Gly 135
Db      406 GTGAAGGACATCTAAACCCCATGCAAGTCCAGAGCTTTCGACACAGCCGGGGA 465
Qy      136 HisGlyGlyAspThrTrpAspTyrTyrSerHisValMetThrIlyrPheAlaGluGlu 155
Db      466 CAGCGAGAGACCGTGGGACACCAAGGCTAGCCCATCAAGATAGAGACCTCTTGAGCCA 525
Qy      156 AspValArgArgSerPheGluAsnThrAlaAlaAspTrpProGluMetGlnThrLeuAla 175
Db      526 GACGAGAGAGCGC-----CCCGAG----- 543
Qy      176 GlyAlaPheAspSerAspArgTrpGlyPheAlrProArgThrValValLeuHisGlyLys 195
Db      544 -----CCACCGCGCACCGTGGTGCATGCGAAGCGCG 573
Qy      196 SerGlyTlleglyLysSerAlaLeuAlaArgArgIleValLeuCytrPAlaGlnGly 215
Db      574 GCAAGGATAGGCAAGTCCATGCTGCGACACAGAGTGAATGCTGAGCTGGCGGACGGGAG 633
Qy      216 LeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet---GlnArg 234
Db      634 CTCTTCAGAGCGAGATTTGATTTATCTCTTCACTCACTGACAGGAGATGAACCAAGT 693
Qy      235 LysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGlnAlaPro 254
Db      694 GCCACGGAATGACATGCAAGACCTCATCTTCACTGCTGCTGCTGAGCCAGCGCGCT 753
Qy      255 ValThrGluIleMetSerArgProGluArgLeuLeuPheIleIleAspGlyPheAspAsp 274
Db      754 CTCAGAGAGTCAATCCAGATTCCCGAGCGCTCTTTCATCATGACGCGCTTGATGAG 813
Qy      275 Leu---GlySerValIleuAsnAspThrTyrLeuLeuCytyAspTrpAlaGlnGluGln 293
Db      814 CTCAGAGCTTCTTCCAGATCTCTCAGAGACCTGTGGCTCTGCTGAGAGAAACCG 873
Qy      294 ProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSerPheLeu 313
Db      874 CCCACGAGAGCTCTTTCACGCTTAATGGAAGAGCTGCTCCCTGAGCTATCTTTG 933
Qy      314 IleValThrValAlaArgAspValGlyThrGluLysLeuLysSerGlnValValSerProArg 333
Db      934 CTCATCACACACACGCGCCACGAGCTTTGAGAGAGCTCCACCGTGTGAGACACCCAG 993
Qy      334 TyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuLeuGluArgGly 353
Db      994 CATGTGAGATCTGGGCTCTTCTGAGGCGAAGAAAGAAAGAAATCTTCAACATATTTTC 1053
Qy      354 IleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAspArgLysLeuLeu 373
Db      1054 CACAAATGACAGACGCGCGGCGGCAAGTCTTCAATTACGTGAGAGCAACAGAGCTCTTTC 1113
Qy      374 AspGlnCytyGlnValProAlaValGlySerLeuIleCytyValAlaLeuGlnLeuGlnAsp 393
Db      1114 ACGATGTGCTTCGTCCTGCTGTGTGCTGTGTGTGTGCTGCTGCTGACAGACACACTG 1173
Qy      394 ValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGlyLeuHisAlaAlaPhe 413
Db      1174 GAGGGTGGGGGCTGTGTGAGACAGACGTCACAGACCAACCTGACGTATACCTCTCTG 1233
Qy      414 ValPheHisGlnLeuThrProArgGlyValValArgArgCytyLeuAsnLeuGluGluArg 433
Db      1234 CTGCTGAGTCTGATGCAACCCAGACCGGCGGCGCGCGC-----CTCAGCGCCCA 1284
Qy      434 ValValLeuLysArgPheCytyArgMetAlaValGluGlyValTrpAsnArgLysSerVal 453

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Db      1285 CCCAACAGAGAGGCTGTGCTCTTGGCGGACAGATGGGCTGTGAATCAAGAAATCTTA 1344
Qy      454 PheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeuArgAlaLeuPhe 473
Db      1345 TTGAGGAGCAGGACCTCCGGAACACAGGCTTGAAGCGGAGAGACGTTCTGCTCTTC 1404
Qy      474 HisMetAsnIleLeuLeuProAspSerHisCytyGluGluLysTyrThrPhePheHisLeu 493
Db      1405 AACATGAACATCTTCCAGAAAGACATCACTGTGAGAGGATATACAGCTTCATCCACTTG 1464
Qy      494 SerLeuGlnAspPheCytyAlaAlaLeuTyrTyrValLeuGlu-----GlyLeu 509
Db      1465 AGTTTCAGAGAAATCTTGTGAGCTATGTACTATATCTTGACAGAGGAGGAGCGGGGCA 1524
Qy      510 GluIleGluProAlaLeuCytyProLeuTyrValGluLys-----ThrLysArgSerMet 527
Db      1525 GGCCCAACACAGACGTGACACAGGCTTTGACCGAGTACCGCTTTTCTGAAGAGCTTC 1584
Qy      528 GluLeuLysGlnAlaGlyPheHisValHisSerLeuTrpMetLysArgPheLeuPheGly 547
Db      1585 -----CTGCACTCAACAGCGCTTCTGTTTGA 1614
Qy      548 LeuValSerGlyAspValArgArgProLeuGluValLeuLeuGlyCytyProValProLeu 567
Db      1615 CTCTGAACGAGAGACACCAAGGACCACTTGGAAGAAGTCTGTGAGAAAGTCTGCGCG 1674
Qy      568 GlyValLysGlnLysLeuLeuHisGTrpValSerLeuLeuGlyGlnGlnProAlaAlaThr 587
Db      1675 CACATCAAGATGGAAGCTGTTGCAAGTGATCAAGCAAGACTGACAGACCGCTCCACC 1734
Qy      588 ThrProGlyAspThrLeuAspAlaPheHisCytyLeuPheGluThrGlnAspLysGluPhe 607
Db      1735 CTGAGAGAGGCTCTTGAAGTCTTTCAGCTGCTTGAACAGATCCAGAGAGAGAGTTT 1794
Qy      608 ValArgLeuAlaLeuAsnSerPheGlnGluValTrpLeuPro---IleAsnGlnAsnLeu 626
Db      1795 ATCCAGAGGCGCTGAGCCACTTCCAGTGATGTGCTGCAACATTCCTCCCAAGAT 1854
Qy      627 AspLeuIleAlaSerSerPheCytyLeuGlnHisCytyProTyrLeuArgLysIleArgVal 646
Db      1855 GAGCAGATGCTCTCTGTTCTGTGTGAAGCGCTGC----- 1890
Qy      647 AspValLysGlyIlePheProArgAspGluSerAlaGlnAlaCytyProValValProLeu 666
Db      1891 -----AGGAGCGCCAGCGTGTCTG----- 1908
Qy      667 TrpMetArgAspLysThrLeuIleGluGluGlnTrpLysAspPheCytySerMetLeuGly 686
Db      1908 ----- 1908
Qy      687 ThrHisProHisLeuArgGlnLeuAspLeuGlySerSerIleLeuThrGluArgAlaMet 706
Db      1909 -----CACTTG-----TATGGCGCCACTCAAGCGGCGAGCGGAGAGAC 1947
Qy      707 LysThrLeuCytyAlaLysLeuArgHisProThrCytyLysIleGlnThrLeuMetPheArg 726
Db      1948 CGCGGAGGTGCTCCGACGAGGCGCAC---ACGCTGTGTGTGAGCTCAGACCAAGAGAG 2004
Qy      727 AsnAlaGlnIleThrProGlyValGlnHisLeuThrArgLysIleValMetAlaAsnArgAsn 746
Db      2005 ACCGTTGTGTGACCGCTACAGTAAACATCTGACAGCGGCGCTGTGACCAATCCAAAC 2064
Qy      747 LeuArgSerLeuAsnLeuGlyGlyThrHisLeuLysGluGluLysValAlaArgMetAlaCyty 766
Db      2065 CTGATAGAGTGTCTCTGTACCGAAAGCGCTGGGACCGGGGGGGTGAAGCTGTCTGT 2124
Qy      767 GluAlaLeuLysHisProLysCytyLeuGluGluSerLeuArgLeuAspCytyGlyLeu 786
Db      2125 CAAGACTACAGACACCCCACTGCAACTCAGAACTGAGAGCTGAAAGAGTGCAGCATC 2184
Qy      787 ThrHisAlaCytyTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSer 806
Db      2185 TCCAGCTCAGCGCTGCGAGACCTCTGTGAGCTCTCATAGCCAAATGAATTTGACAAAG 2244

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Db 730 GCGCACACGAGCTTACAGCCCAACCAACCATGAGAGCCTTCTGTGAGAGAGCCTC 789  
 Qy 139 ---AspThrTrpAspTyrIleYsSerHisValMetThr---LysPhe----- 151  
 Db 790 TGTTCACATAGCCCTGGAAAAATGAGAGATTTTAAACAAAATTTCAACACAGCTCTACTT 849  
 Qy 152 -----AlaGluGluIleAspValAlaArgArgSerPheGluAsnThr 164  
 Db 850 CTACAAAGACCTCACCCCAAGAACCAAGATCCCTGGTCAAGAGAGAC----- 897  
 Qy 165 AlaAlaAspTrpPro----- 948  
 Db 898 -----TGGCCTGATTATGTGAGAGAGATGAGACATTTTAATTAAGATGAGAC 948  
 Qy 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValIleLeu 192  
 Db 949 TTATTGTGACCGAGCCTGGATACCA-----GAACTTCGATATGTACTACTG 996  
 Qy 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTrpAla 212  
 Db 997 CAGGGGCTGCTGGAATTGGAGATCAACACTGGCCAGGAGAGTGAAGAAAGCTGGGGG 1056  
 Qy 213 GlnGlyLysLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232  
 Db 1057 AGAGGCGAGCTGTATGGGAGCCGCTTCAGCATGTCTTCACTTCAGCTGCAGAGAGCTG 1116  
 Qy 233 GlnArgLysLysGlySerValIleLeuAsnAsn---AspThrLysLeuCysValAspTrpAlaGlu 252  
 Db 1117 GCCAGTTCAGAGGTGAGTCTGCTGAGCTCATCGAAAAGATGGAGACGCCATCCG 1176  
 Qy 253 AlaProValThrGluIleMetSerArgProGluArgLeuPheIleIleAspGlyPhe 272  
 Db 1177 GCTCCCATAGACATCTGCTGTAGGCAAGAGCGGCTGCTTCATCTTCGATGAGTGTA 1236  
 Qy 273 AspAspLeuGlySerValIleLeuAsnAsn---AspThrLysLeuCysValAspTrpAlaGlu 291  
 Db 1237 GATGAGCGAGATGAGTCTGTGAGAGCCGAGCTGTCTGTGACTGTGACATGAGACAG 1296  
 Qy 292 LysGlnProPheTrpPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311  
 Db 1297 CCAACGCGCGGAGATGACACTCTGGGCACTTGTCTGGGAAATATATATCTTCCGAGGCA 1356  
 Qy 312 PheLeuIleValIleThrValArgAspValGlyThrGluLysLeuLysSerGlnValValSer 331  
 Db 1357 TCCCTTCATGATCAGGCTCGGACACAGCTGTGAGAAACCTCATCTCTTTGGAGACAG 1416  
 Qy 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisValLeuLeuGlu 351  
 Db 1417 GCAGGTGTGGTGAAGGTCTGGGGTCTGTGAGTCCAGAGAGAAATATTCTACAGA 1476  
 Qy 352 ArgGlyIleGlyGlnHisGlnLysThrGlnLysLeuArgAlaIleMetAsnAsnArgGlu 371  
 Db 1477 TATTTCACATGTAAGGCAAGCAATTAGACCTTTAGGTGGTTCGCAATCAACAAAGAG 1536  
 Qy 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391  
 Db 1537 CTCTGGGCGCTGTGCTTGTGCTGCGGTGTCTGTGCTGAGCTGCATCTGCTGATGACAG 1596  
 Qy 392 GlnAspValValGlyLysSerValAlaProPheAsnGlnThrLeuThrGly-----Leu 409  
 Db 1597 CAGATGAAGCGGAGAAACCTACACTGACTTCAGAACACCAACCAACCTCTGTCTTA 1656  
 Qy 410 HisAlaIlePheValPheHisGlnLeuThrProArgGlyValAlaArgArgCysLeuAsn 429  
 Db 1657 CATTAACCTGCGCAGGCTCTCCAACTCAGGCCATTGGGA----- 1695  
 Qy 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449  
 Db 1696 -----CCCAAGCTCAGAGACCTGTGCTGTGCTGCTGAGGCGATCTGGCAA 1743  
 Qy 450 ArgLysSerValPheAspArgLysAspAspLeuMetValGlnGlyLeuGlyLysSerGluLeu 469  
 Db 1744 AAAAAGACCTTTTCACTGCAGATGACCTCAGAAAGCATGGGTTAGATGGGGCATCATTC 1803

Qy 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGlu 485  
 Db 1804 TCACACCTTCTGAAGATGGATATTCTTCAAGAGACCCCATCCCTGACAC----- 1854  
 Qy 486 GluTyrTyrThrPhePheHisIleLeuSerLeuGlnAspPheCysValAlaIleLeuTyrVal 505  
 Db 1855 -----TACAGCTTCATTCACCTCTGTTCCAAAGTCTTTCAGAAAGTCCATGCT 1908  
 Qy 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCysProLeuTyrValGluLysThr 523  
 Db 1909 TTGAGAGATGAGAAAGGAGAGATTAACATTTCTATGATCATATGATTTGGAAAGACG 1968  
 Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540  
 Db 1969 CTAGAGACA-----TATGAAATATACATGAGCTGTGGGAGCATCA 2007  
 Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValAlaArgProLeuGluValLeu 560  
 Db 2008 ACCACAGTTCCTTATTGGGCTGTTAAGTGAAGGAGAGAGAGATGAGAGATGCATC 2067  
 Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisIleTrpValSerLeuLeu 580  
 Db 2068 TTTCACCTGCGGCTGTCTCAGGG-----AGAACTGATGCAGTGGTCCGCTCCTG 2121  
 Qy 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598  
 Db 2122 CAGCTGCTGTCGAGCCACAC-----TCTCTGAGTCCCTTCACATGCTC 2163  
 Qy 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618  
 Db 2164 TTGTACAGACCTGGAAACCAACGTTCTGTACACAACTGATGAGCCCATTTGAAAGATG 2223  
 Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638  
 Db 2224 GGCATGTGTGTGAAGAAACACATGAGACCTTTGTGTGACATTTCTGCATTAATTACAG 2283  
 Qy 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAla 658  
 Db 2284 CGCACGTAAGAAAGCTTCAGCTG---ATTGAGGGC-----AGGACGACACAGATCA 2331  
 Qy 659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGlnThr 678  
 Db 2332 ACATGAGCCCAACCAAGTATGATTCGTTCAGGGGTCCCAAGTACAGATGCCATTGG 2391  
 Qy 679 GluAspPheCysSerMetLeuGlyThrHisProHisIleuArgGlnLeuAspLeuGlySer 698  
 Db 2391 ----- 2391  
 Qy 699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718  
 Db 2391 ----- 2391  
 Qy 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnIleLeuTrp 738  
 Db 2392 -----CAGATTCTCTTC 2403  
 Qy 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyIleThrHisIleLys 758  
 Db 2404 TCCGTCTCAAGGTCAACCAAACTGTAAGAGACTGGAACCTTAAGTGAACCTGCTGAGACC 2463  
 Qy 759 GlnGluAspValArgMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGluSer 778  
 Db 2464 CACTGTCAAGTGAAGAGTCTTTGTAGACCTGTGAGAGCCCTGCTGCTGCTGAGACCC 2523  
 Qy 779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysIleTyrLeuLysIleSerGlnIleLeu 798  
 Db 2524 CTGGCG----- 2529  
 Qy 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818  
 Db 2530 -----TTGGCTGGC----- 2538





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LOCATION: (1) ..(4422)
US-09-388-221B-1

Alignment Scores:
Pred. No.: 2.94e-85 Length: 4422
Score: 955.00 Matches: 366
Percent Similarity: 38.01% Conservative: 189
Best Local Similarity: 25.07% Mismatches: 438
Query Match: 13.50% Indels: 468
DB: Gaps: 51

US-10-066-521-6 (1-1344) x US-09-388-221B-1 (1-4422)
QY 11 SerTyrGlyLeuGlnTrpCysLeuTyrGlu---LeuAspYsgIuGluPheGlnThrPhe 29
DB 13 GCGTGGGGCCCGCTGGGCTGTACTTGAAGTTCCTGAAGAAGAGAGCTGAAGAGACTTC 72
QY 30 LysGluLeuLeuYslySlySer---SerGluSerThrThrCysSerIleProGlnPhe 48
DB 73 CAGCTTCGTCTCGCAATTAAGCCGACCTCCAGAGGCTCTTCGGGTGAAGACCCGCTCAG 132
QY 49 GluIleGluAsnIlaAsnValGluCysLeuAlaLeuLeuHisGluTyrTyrGlyAla 68
DB 133 CCAAGAGAAGACAGATGGCATAGAGGTGGCTCGTACTGGTGCTCAG---TATGGGAG 189
QY 69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSer 88
DB 190 CAGGGGCTCTGGAGCTTAAGCTCTCATACCTGGAGAGAGATGGGCTGAAGCTCATGTC 249
QY 89 GluLysAlaArgAspAsp----- 94
DB 250 GCCCAAGCCCAAGAAAGGGGAGGCGCACTCTCCATTCCTCAAGCCCAAGTAAACC 309
QY 94 ----- 94
DB 310 CACCTGGGGTCTCCCAAGCAACCACTCCACGCACTGAATGCTTGATCATGA 369
QY 94 ----- 94
DB 370 TTGCGGGGGGGTCAACCAAGGCTCAGAGAAGAAAGGTTTGAAGACAGTCTGACACA 429
QY 95 -----MetLysLysIleSerGlnAlaMet----- 102
DB 430 TCTGAGCGCGCTGAGAGAAATCTGTGCTCACTCTCTCAACAAAGCTTCCAAAGTCC 489
QY 102 ----- 102
DB 490 CCAAGACATGATCTCCAAGCGAAGAGTCAACCAAGCCCAATCATCAAGCATGCTG 549
QY 103 -----GluGlnGluGlyAla--- 107
DB 550 GGGAGCTGGGGATCCCAACTCAGCCAGCTAGACCAAGAGAGAGAGGCTCTGGG 609
QY 108 -----ThrAlaAlaGluThrGluGlu 114
DB 610 ACCCAATGGCTCTGATGAAGAACTCAGAAATTATTAACAAGAAATCAGAGAAAGAG 669
QY 115 GlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGluGln 134
DB 670 AGAGAGAAATCAGAGAAAGAGAGGCGCCCAATGGGACAGGGGTGATGAGAGAGCCCAAG 729
QY 135 GluYHisGlyGly----- 138
DB 730 GCGGACACCAAGCTTAAGAGCCCAACAACCAATGGAGAGCTTCTGTGAGAGAGAGCTC 789
QY 139 ---AspThrTrpAspTyrTyrSerHisValMetThr---LysPhe----- 151
DB 790 TGTTCACATGGCCCTGGAAAAATGAGGATTTTAACCAAAATTCACACAGCTGCTACTT 849
QY 152 -----AlaGluGluGluAspValArgArgSerPheGluAsnThr 164
DB 850 CTACAAAGACTCAACCCCAAGAGCCAGATGCCCTGGTCAAGAGAGAGC----- 897

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QY 165 AlaAlaAspTrpPro-----GluMetGlnThr 173
DB 898 -----TGGCTGATATGTGAGAGAAATCAGAGACATTTAAATTGATCAGAGAC 948
QY 174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeu 192
DB 949 TTAATTGGCCCAAGGCTCGATACCA-----GAACCTGCATATGATCATCTG 996
QY 193 HisGlySerSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCysTyrAla 212
DB 997 CAGGGGCTGCTGGAAATGGAAAGTCAACCTGGCCAGAGGAGGAAAGAAAGCTGGGG 1056
QY 213 GlnGlyGlyLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232
DB 1057 AGAGGCAAGCTGTATGGGAGCCGCTTCACAGATGCTTCTACTACAGCTGCAAGAGCTG 1116
QY 233 GluArgLysGluSerSerValThrGluPheIleSerArgLysTrpProAspSerGln 252
DB 1117 GCCCAAGTCCAAAGGTGGTGAAGTCTCGTGAAGCTCATCGAAAGATGGAGACCACTCCG 1176
QY 253 AlaProValThrGluIleMetSerArgProGluArgLeuPheIleIleAspGlyPhe 272
DB 1177 GCTCCATTAAGACAGATCCTGTAGGCGAGAGGCTGCTTCATCTCATATGATGTA 1236
QY 273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCysLysAspTrpAlaGlu 291
DB 1237 GATGAGCCAGATGGGCTTGTGAGAGAGCCAGAGTGTGAAGCTGTGTGACCTGAGCAG 1296
QY 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311
DB 1297 CCAAGCGGCGGAGATGACATGCTGGGAGATTTGTGGGAAAGAACTATCTCCGAGGCA 1356
QY 312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuYsSerGlnValSer 331
DB 1357 TCCCTCTGATCAAGGCTGGAGACCAAGCTGTGAGAACTCATCTCTTGGAGACAG 1416
QY 332 ProArgTyrLeuLeuValArgGlyIleSerGlyGluGlnArgIleHisLeuLeuGlu 351
DB 1417 GCACTTGGGTGAAGGTCTCGGGTCTCTGAGTCCAGCAGAAAGAAATTTCTACAGA 1476
QY 352 ArgGlyIleGlyGluHisGlnLysThrGlnGlyLeuArgAlaIleMetAsnAsnArgGlu 371
DB 1477 TATTTCACATGAAGGCAAGCAATTAGAGCTTTAGTTGGTTCCTCAATCAACAAAGAG 1536
QY 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391
DB 1537 CTCGGGCGCTGTGTCTGTGCTGCTGGGTCTGCTGAGCTGACATTCCTGATGACAG 1596
QY 392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrLeuThrGly-----Leu 409
DB 1597 CAGATGAAGCGGAAGAAACTCACTGACTTCCAAAGCACCAACCAACCTCTGTCTA 1656
QY 410 HisAlaAlaPheValPheHisGlnLeuThrProArgGlyValValArgArgCysLeuAsn 429
DB 1657 CATTAAGTGGCCCAAGGCTCTCCAAAGCTCAAGCTAGGGA----- 1695
QY 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTyrAsn 449
DB 1696 -----CCCAAGCTCAGAGACTGCTGCTGTGCTGCTGAGGAGCATCTGGCAA 1743
QY 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGluSerGluLeu 469
DB 1744 AAAAAGACCTTTTCACTCACTCAAGATGACTCAGAAAGCATGGTGTGATGGGCGCATCATC 1803
QY 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGlu 485
DB 1804 TCAACCTTTTGAAGATGGTATTTCTCAAGAGACCAACCACTCTGAGAC----- 1854
QY 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505
DB 1855 -----TACAGCTTCATTAACCTGTTCCTCAAGAGATTTCTTGGACAGAAATGCTATGTC 1908
QY 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCysProLeuTyrValGluLysThr 523

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Db      1909 TTGGAGATGAGAGGGGAGAGTAACATCTTAATGATCATAGATTTGAAAAGCG 1968
Qy      524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540
Db      1969 CTAGAACCA-----TATGAAATACATGGCCCTGTCTTGGGGCATCA 2007
Qy      541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560
Db      2008 ACCACAGCTTTCCCTTTGGGCTGTAAAGTATGAGGGGAGAGAGATGAGAACATC 2067
Qy      561 LeuGlyCysProValProLeuGlyValIleGlnLysLeuHisIleTrpValSerLeuLeu 580
Db      2068 TTTCACGTCCGGCTGTCTCAGGGG-----AGCAACTGATGACATGGGTCCCGCTCG 2121
Qy      581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrIleAspAlaPheHisCys 598
Db      2122 CAGCTGCTGTGACGCCACAC-----TCTCTGAGCTCCCTCCACTGC 2163
Qy      599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618
Db      2164 TTGTACAGACTCCGACAAACAACTTCTGTGACACAGATGAGCCCATTTGAAAGAAATG 2223
Qy      619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638
Db      2224 GGCATGTGTATGAAGACAGACATGAGCTTTAGTGTGCACATTTCTGATTAATTCAGC 2283
Qy      639 ProGlyLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerIle 658
Db      2284 CGCCACGTGAAGAAAGCTTCAGCTG-----ATTGAGGGC-----AGGCACACAGATCA 2331
Qy      659 GluIaCysProValIleProLeuTrpMetArgAspLysThrIleGluGluGlnTrp 678
Db      2332 ACAAGAACCCCACTGATGTCTGTTCAGTGGGTCCAGTACAGATGCCATTTGG 2391
Qy      679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLysSer 698
Db      2391 ----- 2391
Qy      699 SerIleLeuThrGluArgAlaMetLysThrLeuCysValIleLysLeuArgHisProThrCys 718
Db      2391 ----- 2391
Qy      719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGluValGlnHisLeuTrp 738
Db      2392 -----CAAGTTCTCTTC 2403
Qy      739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyGlyThrHisLeuLys 758
Db      2404 TCCGTCCTCAAGGTACACCAAGAACTGAAGAGCTGAGACTTAAGTGAAGAACTCGCTGAGC 2463
Qy      759 GluGluAspValArgMetAlaCysGluAlaLeuLysHisIleProLysCysLeuLeuGluSer 778
Db      2464 CACTCTGACGTGAAGAGCTTTGTAAAGACCCCTGAAGACCCCTGCTGCTCTGAGAGCC 2523
Qy      779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysIleLysLeuLysIleSerGlnIleLeu 798
Db      2524 CTGGGG----- 2529
Qy      799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818
Db      2530 -----TTGGCTGGC----- 2538
Qy      819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeu 838
Db      2538 ----- 2538
Qy      839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858
Db      2539 -----TGTGGCTGACAGCTGACAGACCTTGCTTTGGGCTTGAGAGCCAAAC 2592
Qy      859 ArgSerLeuThrHisIleLeuCysIleLeuSerHisAsnSerLeuGlyAsnGlnGlyValAsnLeu 878

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Db      2593 CAGAC----- 2598
Qy      879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898
Db      2598 ----- 2598
Qy      899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrpLeu 918
Db      2599 -----CTG 2601
Qy      919 ThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGlu 938
Db      2602 ACCAGCTGACCTGAGCTTCAATATGTCTACGAGATGCTGAGGCCAAACCTTTGCCAG 2661
Qy      939 ValMetArgGluProSerCysHisIleGlnAspLeuGluLeuValLysCysHisLeuThr 958
Db      2662 AGACTGAGACAGCCGAGCTGACACTACAGAGTACGACGCTGACGCTGAGCTGAGCTCAG 2721
Qy      959 AlaIaCysCysGluSerLeuSerCysValIleSerArgSerArgHisIleLysSerLeu 978
Db      2722 TCTGACTGCTCCAGACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2781
Qy      979 AspLeuThrAspAsnAlaLeuGlyAspGlyValAlaAlaLeuCysGluGluLysLeuLys 998
Db      2782 GACCTGACAGACAAACACCTGATGACGTTGGCTGACGCTCTGTGTGTGTGTGTGTGTGTGT 2841
Qy      999 GlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCysGlyLeuThrSerAspCys 1018
Db      2842 CATCTGCTGCTCAAACTATACGCTGTGGGCTTGACACAGAACCTTGAAGTATGAGATG 2901
Qy      1019 CysGlnAlaLeuSerLeu-----AlaLeuSerCysAsnArgHis 1031
Db      2902 AGCGAGAACTGAGGGCCCTGAGACAGAGAAACCTCAGCTGCTCATCTTCACTGACAGAG 2961
Qy      1032 LeuThrSerLeu-----AsnLeuValGlnAsnAspPhe 1042
Db      2962 AAACCAAGTGTGATGACCTTACTGAGGGCTGTGATACGGAGAGATGATGATTAATGACA 3021
Qy      1043 SerProLysGlyMetMetLysLeuCysSerAlaPheAlaCys-----ProThrSer 1059
Db      3022 TCTTCACCTCAAGCCGACAGACTCGGATCAGAGAGGGGCTTCCCATGTTGCTCAGGCT 3081
Qy      1060 AsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTrpProValGlnIleArgLysLeuLeu 1079
Db      3082 AATCTCAAACTCTGACAGCTGAGCAAG-----ATCTTCCA-----ATTGCTGAGATTGCA 3132
Qy      1080 GluGlu-----ValGlnLeuLeu-----LysProArgValIle 1091
Db      3133 GAGGAAGCTCCCAAGAGTAGTACCGGTGAACTCTGTGCGCTGCTTCTCTGCTCTCT 3192
Qy      1092 AspGlySerTrpHisSerPheAspGluAspArgHisIleLysIle-GlyLeuThrPheArg 1111
Db      3193 CAAGGAGACCTGCAATAC-----AGCCTTTGGGACCTGACGATGAC 3234
Qy      1111 GlnProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProGluGlnLys 1131
Db      3235 TTTCGGGGCCCAAGGGGC-----CTGTGGCTACTAGAGTATTGACAAA 3279
Qy      1131 GlyArgValSerLeuLeuAlaGlyAspPheLysSerSerThrArgPheAlaLysSerIle 1151
Db      3280 GAAAAA-----ACTGTATCCGAGTTCACT--TCCCT 3309
Qy      1151 CysLeuAlaThrAlaAsnGlyLysSerGlnArgValAspAsnVal-GluGlnSerSerP 1171
Db      3310 GTAAGTGGCTCTTACCGCTGGCCCAACA-----CGGGTCTCTGTTTGTGATGAGAAAGC 3366
Qy      1171 ArgIleProMetAlaGlyThrGlnHisLysGlnAspLysMetLeuSerValGly--TrpS 1190
Db      3367 GTGAC-----CCTTGAGATTGAATCTGTGTGTGAGCAACAGATTC 3405
Qy      1190 ArgIleAlaTrpSerGluThrAlaGluLeuGluGlyLeuGlySerHisSerSerAlaPheHis 1210
Db      3406 CTGGGTGAGATCAACCCACAGACACAGCTGAGTGT--GGCAGGGCTCTGTGAGATTC 3462

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QY	332	ProkngyrtleuLeuValAarglyTlaseSgLygluInlrgTlenthleuLeuLeuGlu	351
Db	1939	GCACGTGGGAGAGAGGCTCTGGGGGTTCTTCAGTCCGACGAGAAAGAAATTTCTACAGA	1998
QY	352	ArgGlyTllegLygluInlsgInlYsThrcInglYleuAArgAlaleuAenAenAArgGlu	371
Db	1999	TATTTACAGATGAAAGGCAAGCAATTAAGAGCCTTAAGGTTGGTTGGCAATCAAAACAGAG	2058
QY	372	LeuLeuAenArgInCyegInlValProAlaValGlyserLeuTleCyValAlaleuGlnLeu	391
Db	2059	CTCTGGGCGCCGTGTCTGTGCGCTGGGGGTGCTCCGGTGGCGCTGACCTTCGATGAGAG	2118
QY	392	GlnAenValValGlygluSerValAlaProPheAenGlnThrLeuThrGly-----Leu	409
Db	2119	CAGATGAAGCGGAAGAAATACTACACTAGCTTCCAGAACACACACACACACCTGTGTCTA	2178
QY	410	HisAlaAlaPheValPheNlsgInleuThrProArgGlyValValAargArgCyValAen	429
Db	2179	CATTACCTTGGCCGAGCTCTCCAGCTCAGACCATTTGGGA-----	2217
QY	430	LeuGlnGlnAargValValleuLYaArgPheCyAArgMetAlaValGlnGlyValTPrAsn	449
Db	2218	-----CCCGAGCTGAGACCTCTGCTCTGTGGTGGCTGAGGGCATTTGGCA	2265
QY	450	ArgLySerValPheAenArgLYaSPArgLeuMetValGlnGlyLeuGlygluSerGluLeu	469
Db	2266	AAAAAGACCTTTTCAGTCCAGATGACCTTCAGAAAGCATGGGTTAAGATGGGGCATATGC	2325
QY	470	ArgAlaLeuPheNlsmetAenlleu-----LeuProAenSerHisCyGlu	485
Db	2326	TCCACCTTCTGAAGATGGGTATTTCTTCAGAGACCCCAACCCCTCTGAGC-----	2376
QY	486	GlnYrTyrThrPhePheHisLeuSerLeuGlnAenPheCyValAlaLeuTyrTyrVal	505
Db	2377	-----TACACTTCATTCACCTCTGTTCCAAAGTCTTTGAGAAAGTCTTAATGTC	2430
QY	506	LeuGlnGlyLeuGlu-----TllegInProAlaleuCyProLeuTyrValGlnYlThr	523
Db	2431	TTGGAGATGAGAAAGGAGAGAGATGAACATTTCAATTCACATAGATTTGGAAAAAGCG	2490
QY	524	LYaAenSerMetGluLeuLYeGlnAlaGlyPheNlsgInleuThrLeuTyr-----	540
Db	2491	CTAGAGCA-----TATGAAATACATGGCTGTTTGGGGCATCA	2529
QY	541	MetLYaArgPheLeuPheGlyLeuValSerGlnAenArgValAargArgProLeuGlnValLeu	560
Db	2530	ACCAACAGTTCTCTATGGGCTGTTAAGTATGATGAGGGGAGAGAGATGAGAAATGC	2589
QY	561	LeuGlyCyProValProLeuGlyValYlsgInlyLYeLeuNlsgTPrValSerLeuLeu	580
Db	2590	TTTCACTCCCGGTGTCTCAAGGG-----AGGAACGTAGACAGTGGTGTCCGTCTGTG	2643
QY	581	Gly-----GlnGlnProAenAlaThrThrProGlyAenThrLeuAenAlaPheHisCyS	598
Db	2644	CAGCTGCTGCTGACCAAC-----TCTCTGAGTCCCTGCACATGC	2685
QY	599	LeuPheGlnThrGlnAenArgLYeGlnPheValArgLeuAlaleuAenSerPheGlnGlyVal	618
Db	2686	TTGTTCGAGAGCTCGGAAACAAACGTTCTTCGACACAAAGTAAAGGGCCATTTGGAAGAAATG	2745
QY	619	TrpLeuProTlaleuGlnAenLeuAenArgleuTlaleuAenSerPheCyValGlnHisCyS	638
Db	2746	GGCATGTGTGTGAACACACACATGAGGCTTTAGTGTGCACCTTTCTGCATTAAATTCAGC	2805
QY	639	ProTyrLeuAargLYeAlaArgValAenArgLYeGlyTllepheProAargSPgluSerAla	658
Db	2806	CGCCACGTGAAGAACTTCAGCTG---ATTAGGGC-----AGCAGACACAGATCA	2853
QY	659	GlnAlaCySProValValProLeuTyrMetAargAenArgYsThrLeuTllegInGlnGlnThr	678
Db	2854	ACATGAGCCCAACAGTGTATCTCTTTCAGTGGTGGTCCAGTACACAGTCCATATGG	2913

QY	679	GIuSRpHeCySvSeSerMetLeuGIyThrNiSPRoNiVleuKrgGlnLeuSRleuGIySer	698
Db	2913	-----	2913
QY	699	SeRileuThrGIuARgAlaMetuYThReuCySaLaLySeuKrgNiSPRoThrCyS	718
Db	2913	-----	2913
QY	719	LySileGlnThReuMetPheARgAsnAlGlnIleThRProGlyValGlnIleuThR	738
Db	2914	-----CAGATTCTCTTC	2925
QY	739	ArgIleValMetAlaAsnAlaGAsnLeuARgSerLeuAsnLeuGIyThRNiSeuLyS	758
Db	2926	TCGCTGCACAGTCAACGAAACCTGAAGAGAGCTGAGCTTAAGTGAACCTCGCTGAGC	2985
QY	759	GIuGIuARValARgMetAlaCySGuAlaLeuLySniSPRoLySvSeuLeuGIuSer	778
Db	2986	CACCTGCAGTGAAGAGAGCTTTGTGAACCTGTGAAGAGCCCTCGCTGCCCTCGTGAAC	3045
QY	779	LeuARgLeuARCySvGIyLeuThRniAlaCySTyLeuLySileSerGlnIleu	798
Db	3046	CTGGCGG-----	3051
QY	799	ThrThRSeRProSeRLeuLySSeRLeuSeRLeuAlaLyAsnLySValThRARgGlnLy	818
Db	3052	-----TTGGCTTGCG-----	3060
QY	819	ValMetProLeuSeARPaLaLeuARValSeRGIuCySaLaLeuGlnLySeuIleu	838
Db	3060	-----	3060
QY	839	GIuARCySvGIyIleThRAlaThRGIyCySGInSeRLeuAlaSeRAlaLeuValSeARn	858
Db	3061	-----TGTGGCTTCACAGCTGAGAGACTGGAAGAGACTTGCTTGGGCTGAGAGCCAAC	3114
QY	859	ARgSeRLeuThRniSeuCyvSeuSeRAsnSeRLeuGIyAsnGIuGIyAlaAsnLeu	878
Db	3115	CAGACC-----	3120
QY	879	LeuCyvARgSeRMetARgLeuProNiCySeSerLeuGlnARgLeuMetLeuAsnGlnCyS	898
Db	3120	-----	3120
QY	899	HisLeuARThRAlaGIyCySvGIyPheLeuAlaLeuAlaLeuMetGIyAsnSeRTyPLeu	918
Db	3121	-----CTG	3123
QY	919	ThRniSeuSeRLeuSeRMetAsnProValGIuARAsnGIyValLySeuLeuCySvGIu	938
Db	3124	ACCGAGCTGAGACTGAAGCTTCAATGTGCTCAGGATGCTGGAGGCCAAACCTTTGGCAG	3183
QY	939	ValMetAlaGIuProSeRSeCyHniSeuGlnARgLeuGlnuSeuValLySvHniSeuThR	958
Db	3184	AGACTGAGACGCGAGCTGCAACCTCAAGAGACTGAGAGCTGAGCTGAGCTGAGGCTCAAG	3243
QY	959	AlaAlaCySvSGInSeRLeuSeCyValIleSeRARgSeRAlaGhiSeuLySeRLeu	978
Db	3244	TCTGACTCTCTCCAGAGACTGCTCTGTCTGTACTGCCAGCCCCAGCTGAAGAGACTA	3303
QY	979	AspLeuThRAspAsnAlaLeuGIyARSPLyGIyValAlaAlaLeuCySvGIuGIyLeuLyS	998
Db	3304	GACCTGAGACGAGAACCTGAGATGACCTTGCGCTGCGAGACTCTGTGAGAGGCTCAAG	3363
QY	999	GlnLyAsnSeRValLeuThRARgLeuGIyLeuLySAlaCySvGIyLeuThRSeRSPCyS	1018
Db	3364	CATCTGCCTGCMAACTATACGCTCGGGCTGACACAGAACACTCTGAGTATGATGCTG	3423
QY	1019	CysGIuAlaLeuSeRLeu-----AlaLeuSeRCySAsnARgHiS	1031
Db	3424	AGCGAGAACTGAAGGCGCTTGAGACGAGAAACCTCAAGCTGCTCATCTTCAGACGAGCG	3483
QY	1032	LeuThRSeRLeu-----AsnLeuValGlnAsnAsnPhe	1042

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Db      3484 AAACCAAGTGTATGACCCTACTGAGGGCTGTGATACGGGAGAGATGATTAATAGACA 3543
Qy      1043 SerProlyseGlyMetethyleuCySerAlaPheAlaCyS-----ProthSer 1059
Db      3544 TCTCTCACTCAAGCGCGCAGAGACTCGGATCGAGAGCGCGCTTCCATGTGTCTCAGGCT 3603
Qy      1060 AAmLeuGlnIleIleGlyLeuTrpGlyTrpGlnTrpValGlnIleArgLysLeu 1079
Db      3604 AATCTCAACTCTCTGACGTGACAG--ATCTTCCA-----ATTGCTGAGATTGCA 3654
Qy      1080 GluGlu-----ValGlnLeu-----LysProArgValIle 1091
Db      3655 GAGAAAGCTCCCAAGAGTAGTACCGGTGAACCTTGCGCGCTCTCTCTGCTCT 3714
Qy      1092 AspGlySerTrpHisSerPheAspGluAspAspArgHisLysIle-GlyLeuThrPheAr 1111
Db      3715 CAAGGGGACCTGATAG-----AAGCCTTGGGGAGCTGACGATGAC 3756
Qy      1111 GluLeuProGluSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnProGluGln 1131
Db      3757 TTCTGGGGGCCCCACGAGGC-----CTGTGCTACTGAGTACGATGACAA 3801
Qy      1131 sLyAspValSerLeuLeuAlaGlyAspPheLysSerSerThrArgPheAlaLysSerIle 1151
Db      3802 GAAAGA-----ACTTGACGAGTTCACT---TCCCT 3831
Qy      1151 uCyLeuAlaThrAlaAsnGlyLeuSerGlnArgValAspAsnVal-GluGlnSerSerP 1171
Db      3832 GTAGCTGGCTCCACCGCTGGCCCAACA---CGGGTCTGCTTGTGTTGAGAGAAAGCG 3888
Qy      1171 roGlnProMetAlaGlyThrGlnHisLysGlnAspLysMetLeuSerValGly---TyrS 1190
Db      3889 GTGAC-----CGTGAATTAATTTCTGTGTGGACCACTTC 3927
Qy      1190 exGlyAlaTrpSerGlnThrAlaGluGlnGlyLeuGlySerAsnSerAlaAspHisA 1210
Db      3928 CTGGGTGATGATCAACCAACAGACAGCTGATGT---GGCAGGGCTCTGTGTCAGATC 3984
Qy      1210 sPHisGlyGlyMetAlaTrpSerLeuGlyArgGluLeuSerSerArgGlyLeuCyS---- 1228
Db      3985 AA-----GGCTGAGCTGTGAGCTGTGA---AGCTGTGACCTCCCTCACTTGTGGCT 4035
Qy      1229 --ProthValLeuMetThrThrAlaValCysProGlyHisLysTrpGluArgLeuGlySera 1248
Db      4036 CTCCAAGGGG--GCCATGTGACACATCCCTCT---TCCAATGGCCCACTTTAAAGGA 4091
Qy      1248 rGgLy----- 1249
Db      4092 GGGGATGCTCTGGAGAAAGCCAGCCAGGTGAGCTGATCATCATAGTTCTGAAACC 4151
Qy      1249 ----- 1249
Db      4152 CAGCTTCTCCCTTGGAGTCTCTGAAATGATTCATATGCTCGGCTTCATTC 4211
Qy      1250 -----TrpCyS-----LeuAsnSerAlaAspAspHis 1259
Db      4212 CGTCACTCTGTGTGTGTGTTTACACACCGCTTCATCTGAGGAATCATCTCCACCT 4271
Qy      1259 er-----GlyValSerTrpSerLeuGlyAlaIleGlyL 1270
Db      4272 CTACCTGATCCCAAGTACTGCTTCATTCGGAAGAGACTGAGC-----TCTGCTA 4322
Qy      1270 euGlnGlyLeuValSerAsnSerAlaAspAspHisSerGlyValAla---TrpSerLeuG 1289
Db      4323 TCGAAGCCCTGGAGAGACAGCTGTTCTCGAGTTCTACGTTGCGCACTTGGGATGACG 4382
Qy      1289 lYala-Ala-----GlyLeuGlnGlyLeu----- 1296
Db      4383 GATGAGCTGCAAGTGAAGACAAAGAAATGACATCTGTGTGTGGAGGCTTGTGGAA 4442
Qy      1297 -----ValSerAsnSerAlaAspAspHisSerGly----- 1306

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Db      4443 ACCAGAGATCTGATCGTCAACTACTGTGATCCCTCCAGCCCGATAGCCGTACTTC 4502
Qy      1307 ValSerTrpSerLeuGlyAlaIleGlyLeuValSerAsnSerAlaAspAsp 1326
Db      4503 ACCTGTGATGCCCCCGCAGTGTGCTGACATTGTGACACAGTATCGAGAGCTGATAGC 4562
Qy      1327 HisSerGlyValSerTrpSerLeu 1334
Db      4563 CCGAGTGACATCGG--TGGAGGTTG 4585

RESULT 6
US-09-388-221B-3
; Sequence 3, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ. ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4200
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4197)
; US-09-388-221B-3

Alignment Scores:
Pred. No.: 1,08e-84 Length: 4200
Score: 949.00 Matches: 387
Percent Similarity: 35.79% Conservative: 190
Best Local Similarity: 24.01% Mismatches: 458
Query Match: 13.42% Indels: 579
DB: Gaps: 55

US-10-066-521-6 (1-1344) x US-09-388-221B-3 (1-4200)
Qy      11 SerTrpGlyLeuGlnTrpCySLeuTrpGly---LeuAspLysGluGlnPheGlnThrPhe 29
Db      13 GCCTGGGGCGCGCTGGCTGTGTTACTTGAGTCTCTGAAGAGAGAGCTGAGAGCTTC 72
Qy      30 LysGlnLeuLeuLysLysLysSer---SerGluSerThrThrCysSerIleProGlnPhe 48
Db      73 CAGCTTGTGCTCGCAATTAAGCGCACTCCAGAGGCTTTCGGGTGAGACACCCGCTCAG 132
Qy      49 GluIleGluAsnAlaAsnValGluCySLeuAlaLeuLeuLeuHisGlyTrpGlyAla 68
Db      133 CAGAGAAAGACGATGACATGAGGTGGCTCGTACCTGTGGCTCAG---TATGGGAG 189
Qy      69 SerLeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetLeuLeuAlaGlnTrpLeuSer 88
Db      190 CAGCGGCTTGGGACCTTGAAGCTTCATACCTGGAGGACATGGGGCTGAGGTCACTGTGC 249
Qy      89 GluLysAlaArgAspAsp----- 94
Db      250 GCCAAGCCAGAGAGGGGAGCGGCACTTCCTTCATTCCTTCACGCCAAGTGAACC 309
Qy      94 ----- 94
Db      310 CACTGGGATCTCCACGCAACCAACCTGCACCGCAGTGTAAATGCCCTGATTCATGAA 369
Qy      94 ----- 94
Db      370 TTGCGCGGGGGTGCACCCAGGCTCAGAGAGAGGTTTGTAGACAGCTGACACA 429
Qy      95 -----MetLysLysIleSerGlnAlaMet----- 102
Db      430 TCTGAGCGCGCTGAGAGAAATCTTGCTCTCACTCTTAACCAAGCTTCCAAAGCTCC 489

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102 ----- 102  
Db 490 CAGACCATGAGTCTCCAGCAGAGTCAACCCCAATCCACAGCAGTCTG 549  
Qy 103 ----- GluGlnGluGlyAla--- 107  
Db 550 GGGAGCTGGGGATCCCACTCAGCCCGCTAGACCCAGAGAGAGGCTCTGGG 609  
Qy 108 ----- ThrAlaAlaGluThrGluGlu 114  
Db 610 ACCCAATGGCTCTGATGAACCTCAGAAATTACTACAGAAATCAGAAAGAG 669  
Qy 115 GlnGluIleSerGlnAlaMetGluGlnGluGlyAlaThrAlaAlaGluThrGluGln 134  
Db 670 AGAGAGAAATCAGAGAAAGCAGAGCCCAATGGCAGCGGTGATGAGAACCCCCACAG 729  
Qy 135 GlyHisGlyGly----- 138  
Db 730 GCGCACACAGCCTACAGCCCAACCAACCATGGAGCCTCTGTGAGAGAGCCTC 789  
Qy 139 ---AspThrTrpAspTyrTyrSerHisValMetThr---LysPhe----- 151  
Db 790 TGTTCACATGGCCCTGGAATAATGAGAGATTTTAAACAAAATTCACACAGCTCTACTT 849  
Qy 152 -----AlaGluGluGluAspValArgArgSerPheGluAsnThr 164  
Db 850 CTACAAAGACCTCAACCCCAAGCCAGAGATCCCTGTGTAAGAGAGC----- 897  
Qy 165 AlaAlaAspTrpPro-----AlaMetGlnThr 173  
Db 898 -----TGGCCGATTAATGTGAGAGAGATCAGAGACATTTAATTGATGATCAGAGAC 948  
Qy 174 LeuAlaGly---AlaPheAspSerPheArgTrpGlyPheArgProArgThrValValLeu 192  
Db 949 TTATTGGCCCAAGCCTGATACCA-----GAACCTCGCATGATCACTACTG 996  
Qy 193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgGlyIleValLeuCysTrpAla 212  
Db 997 CAGGGGGCTGCTGGAAATTTGGAGATCACTGGCCAGGCAAGTAAAGAAAGCCCTGGGG 1056  
Qy 213 GlnGlyLysLeuTyrGlnGlyMetPheSerTyrValPhePheLeuProValArgGluMet 232  
Db 1057 AGAGGCCAGCTGTATGGGAGCCGCTTCAGCATGCTTCACTTCACTGAGAGAGCTG 1116  
Qy 233 GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGln 252  
Db 1117 GCCCAAGTCCAGAGTGTGATGCTCGCTGATCGGAAAGAGAGGAGCCCACTCG 1176  
Qy 253 AlaProValThrGluIleMetSerArgProGluArgLeuPheIleAspGlyPhe 272  
Db 1177 GCTCCCATTAAGACAGATCTGTCTAGCCAGAGCGGCTGCTCTTCATCTCTGATGCTGTA 1236  
Qy 273 AspAspLeuGlySerValLeuAsnAsn---AspThrLysLeuCysLysAspTrpAlaGlu 291  
Db 1237 GATAGGCCAGAGATGGGTCTTGACAGAGCCGAGTTCTGAGCTCTGTCACTGAGAGCCAG 1296  
Qy 292 LysGlnProProPheThrLeuIleArgSerLeuLeuArgLysValLeuLeuProGluSer 311  
Db 1297 CCACAGCCGCGGAGTGCACCTGTGGCAGTTTGTGGGAAACATATCTTCCCAAGGCA 1356  
Qy 312 PheLeuIleValThrValArgAspValGlyThrGluLysLeuLysSerGlyValValSer 331  
Db 1357 TCTCTTCGATCAAGGCTGGACACAGCTTGCAGAACTTATTCCTTTTGGAGCAG 1416  
Qy 332 ProArgTyrLeuLeuValArgGlyLysSerGlyGlnArgGlnIleLeuLeuLeuGlu 351  
Db 1417 GCACCTTGGGTAGAGTCTGTGGGCTTCTGTAGTCCAGAGAGAGAAATATTCTACAGA 1476  
Qy 352 ArgGlyIleGlyLysGlnIleGlnLysThrGlnGlyLeuAlaIleMetAsnAsnArgGlu 371  
Db 1477 TATTTACAGATGAAAGCAGCAATTAAGACCTTAGAGCTTAGTGTGCTTCAAAACAAAG 1536  
Qy 372 LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnLeu 391

Db 1537 CTCTGGGCCCTGTGTCTTGTGCTGCTGGGTCTGCTGGCTGACCTTGATGACAG 1596  
Qy 392 GlnAspValValGlyGluSerValAlaProPheAsnGlnThrGly-----Leu 409  
Db 1597 CAGATGAAGCGGAAGAAATCTACATGACTTCCAGACACCAACCAACCTCTGTGCTA 1656  
Qy 410 HisAlaIlePheValPheHisGlnLeuThrProArgLysValValArgArgCysLeuAsn 429  
Db 1657 CATTAACCTTGCCAGGCTCTCCAAAGCTCAGCAATTTGGGA----- 1695  
Qy 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGlyValTrpAsn 449  
Db 1696 -----CCCAAGCTCAGAGACCTGCTGTGCTGGTGGTGGAGGATGGGCA 1743  
Qy 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyLysSerGluLeu 469  
Db 1744 AAAAAGACCTTTCACTCCAGATGACCTCAGAAAGCATGGGTAGATGGGCCATCATC 1803  
Qy 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGlu 485  
Db 1804 TCACCTTCTTGAAGATGGATTTCTTCAAGAGACCCCACTCCCTGAGC----- 1854  
Qy 486 GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysAlaAlaLeuTyrVal 505  
Db 1855 ---TACAGCTTCACTCACTCTGTTCCAGAGATTTTGGACAGCATGCTCTATGTC 1908  
Qy 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCysProLeuTyrValGluLysThr 523  
Db 1909 TTGAGAGATGAGAGGGGAGAGATTAACATTTCAATGATCATATGATTTGAAAGACG 1968  
Qy 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrp----- 540  
Db 1969 CTAGAGAG-----TATGATATACATGGCTGTGTTGGGACATCA 2007  
Qy 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu 560  
Db 2008 ACCACAGCTTCTTATGGGCTGTAAATGATAGAGGGGAGAGAGATGAGAAACATC 2067  
Qy 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuIleTrpValSerLeuLeu 580  
Db 2068 TTTCACTGCGCGCTGTCAAGGG-----AGAACTGAGACAGTGGTCCCTGCTG 2121  
Qy 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598  
Db 2122 CAGCTGCTGCTCAGACAC-----TCTCGAGCTCCCTCAGCTGC 2163  
Qy 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618  
Db 2164 TTGTACAGAGACTCGGAACAAACGTTCTGTACACAAAGTATGGCCCATTTGAAAGAAATG 2223  
Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638  
Db 2224 GGCATGTGTATGAACACAGATGAGCTTTAGTGTGCACTTTCTTGATTAATTCAGC 2283  
Qy 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProArgAspGluSerAla 658  
Db 2284 CGCCACGGGAAGAGCTTCACTG-----ATTAGAGC-----AGCAGACAGATCA 2331  
Qy 659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGlnGlnTrp 678  
Db 2332 ACATGAGGCCACACATGATGTCTGTGAGGGGGGCCAGTCAAGATGCTATTTGG 2391  
Qy 679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuAlaGlnLeuAspLeuLysSer 698  
Db 2391 ----- 2391  
Qy 699 SerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718  
Db 2391 ----- 2391  
Qy 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp 738



[illegible]

QY	1069	pcIntYrProValGlnIleArgLYsLeuLeuGlnGluValGlnIleuLeuYrProArGva	1089
Db	3130	-----	3130
QY	1089	IValIleAspLYseTrpHisserPheAspGlnAspArghIstlysvIleGlyLeuTh	1109
Db	3131	-----	3138
QY	1109	rPheArgLeuProGlnIserArghIatTrpProCysAlaLeuLeuTrpGlyMetAsnProG	1129
Db	3139	GATGACTTCGGGGGCCCGGGG-----CTGGGGCTACTGAGGTAGTT	3183
QY	1129	uGlnIlyLeuArgValIserLeuLeuIlaGlyAspPheLYseSerThrArgPheAlaIly	1149
Db	3184	GACAAAGAAAAG-----ACTGTACCGAGTCACT--	3214
QY	1149	sSerLeuCysLeuAlaThrAlaenGlyIuSerGlnArgValaAspArhVal-GluGlns	1169
Db	3215	-TCCCTGGTAGTGGCTCTACCGCTGGCCCAAC--CGGGTCTCTGGCTTTGTGTATGAGA	3270
QY	1169	erSerProGlnProMetAlaGlyThrGlnIstlyGlnAspLYseMetLeuSerValGlyI	1188
Db	3271	GAAGCGGTGAC-----CGTTAGATGAAATCTGTGTGTGGAC	3309
QY	1189	--TyrSerGlyAlaTrpSerGlnThrAlaGlnGlnGlyLeuGlyIserAsnSerAla	1208
Db	3310	CAGTTCCTGGGTGAGATACACCCAGACACAGCTGGATGGT--GCCAGGGCTCTCTGG	3366
QY	1208	sPHisAspHisGlyIyMerAlaTrpSerLeuGlyArgGlyLeuSerSerArgLYseu	1228
Db	3367	GACATCA--GGGTGAGCCTGGAGCTGTGA--AGCTTGACCTTCCTCACTTT	3417
QY	1228	ys-----ProThyValLeuMetThrThrAlaValCysProGlyIstIroGlnArgLeu	1246
Db	3418	GTGGCTCTCCAAAGGG--GCCATGTGACATCTCTGT--TCCAAATGGCCCACTTAA	3473
QY	1246	lySerArgGly-----	1249
Db	3474	AGAGAGAGGGAGTGGCTCGAGAGAACCCAGGAGGTGAGCTGATCACAATAGTTTGA	3533
QY	1249	-----	1249
Db	3534	AAACCCAGCTTCCCCCTGGAGAGCTCTGTAAATGATCATTAATGCCCTG	3593
QY	1250	-----TrpCys-----LeuAsnSerAlaAsp	1257
Db	3594	CATTCCCGTCACCTGTGTGTGTGTCTTACACCGGTGCATCTGAGAAAGTCACTT	3653
QY	1257	sPHisSer-----GlyValSerTrpSerLeuGlyAla	1268
Db	3654	CCACCTCACTGTATCCCAAGTGAATGCTCTCATTCGGAAAGAACTGGAGC-----T	3704
QY	1268	IaGlyLeuGlnGlyLeuValserAsnSerAlaAspArhIserGlyValAla---TrpS	1287
Db	3705	CTGTATGAAAGCCCTGGAGAAAGACACAGCTGTTCTGGAGTTTACGTGGCCACTGG	3764
QY	1287	erLeuGlyAlaAla-----GlyLeuGlnGlyLeu	1296
Db	3765	ATCAGAGATCAAGGCTGCAAGTGAAGAACAAGAAAGATGACCTGGTGTGTGGAGGCTT	3824
QY	1297	-----ValserAsnSerAlaAspArhIserGly	1306
Db	3825	GGTGAACACAGAGATTCATGCTGCAACTACTGTATCCCTCCAGCCCGCAATGGCT	3884
QY	1307	-----ValSerTrpSerLeuGlyAlaIlaGlyLeuGlnGlyLeuValserAsnSerAla	1324
Db	3885	ACCTTCACTCTGTGATGGCCGAGTTGCTGCATCTTGTGACCAAGATATGACAGGACGT	3944
QY	1325	AspArhHisserGlyValSerTrpSerLeu	1334
Db	3945	GATAGCCGAGTGCATGCG--TGAAGGTGTG	3973



QY 430 LeuGluGluArgValValLeuLysArgPheCysArgMetAlaValGluGluValTTPAsn 449  
 Db 1696 -----CCCCAGCTCAAGAGACCTTGGCTCTTGGCTGTGGAGCATCTGGCAA 1743  
 QY 450 ArgLysSerValPheAspGlyAspAspLeuMetValGlnGlyLeuGlyGlySerGluLeu 469  
 Db 1744 AAAAAGACCTTTTCACTCCAGATGACCTCAGGAAGCATGGTTTAAATGGGGCATATC 1803  
 QY 470 ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGlu 485  
 Db 1804 TCCAGCTTCTTGAAGATGGATATTCTTCAAGAGCAACCCCATCCCTCTGAC----- 1854  
 QY 486 GluTyrTyrThrPhePheHisIleuSerLeuGlnAspPheCysAlaAlaLeuTyrTyrVal 505  
 Db 1855 -----TACAGCTTCACTTCACTCTGTCTTCCAAAGATTTCTTGCAGAAATCTATATC 1908  
 QY 506 LeuGluGlyLeuGlu-----IleGluProAlaLeuCysProLeuTyrValGluLysThr 523  
 Db 1909 TTGGAGGATGAGAAGGGAGAGAGGTAACATTCTTAATTGCATCATATTTGAAAAGACG 1968  
 QY 524 LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTyr----- 540  
 Db 1969 CTAGAAGCA-----TATGGATACATAGGCTGTGGGGGAGCATCA 2007  
 QY 541 MetLysArgPheLeuPheGlyLeuValSerGluAspValAlaArgPheProLeuGluValLeu 560  
 Db 2008 ACCACAGGTTTCCATTATGGGCTGTATGGATGAGGGAGAGAGAGAGATGAGAAATC 2067  
 QY 561 LeuGlyCysProValProLeuGlyValLysGlnLysLeuLeuHisIleTyrValSerLeuLeu 580  
 Db 2068 TTTCACGTCCGGGGTGTCCAGGGG-----AGAAACCTGATGAGCGGTCCGCTCCCTG 2121  
 QY 581 Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisCys 598  
 Db 2122 CAGCTGTGTGTGAGCCACAC-----TCTCGAGTCCCTCTCCACTGC 2163  
 QY 599 LeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618  
 Db 2164 TTGTACAGACTCGGAACAAACCTTCTGACACAAATGATGGCCATTTCGAAAGAAATG 2223  
 QY 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638  
 Db 2224 GGATGTGTGTGAAGAACAGACATGACCTTATGTGACATTTCTGCATTAATATCAGC 2283  
 QY 639 ProTyrLeuArgLysIleArgValAspValLysGlyIlePheProAlaAspGlySerAla 658  
 Db 2284 CGGCACCTGAAGAGCTTCAAGCTG--ATTGAGGGC-----AGGCAGACAGATCA 2331  
 QY 659 GluAlaCysProValValProLeuTrpMetArgAspLysThrLeuIleGluGluGlnTyr 678  
 Db 2332 ACATGAGGCCCCACCATGTAGTCTGTCAAGTGGGTCCACATGACAGATGCTATATGG 2391  
 QY 679 GluAspPheCysSerMetLeuGlyThrHisProHisLeuArgGlnLeuAspLeuGlySer 698  
 Db 2391 ----- 2391  
 QY 699 SerIleLeuThrGluAlaGlnAlaMetLysThrLeuCysAlaLysLeuArgHisProThrCys 718  
 Db 2391 ----- 2391  
 QY 719 LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValAlaGlnHisLeuTyr 738  
 Db 2392 -----CAGATTCTCTTC 2403  
 QY 739 ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGlyTyrThrHisLeuLys 758  
 Db 2404 TCCGTCTCAAGGTCACACAGAACTGAAGAGCTGAGCTAAATGTGAAGAACTCCGTAGC 2463  
 QY 759 GluGluAspValAlaGlyMetAlaCysGluAlaLeuLysHisProLysCysLeuLeuGlnSer 778  
 Db 2464 CACTCTCAAGTGAAGAGCTTTTGTAAAGCCCTGAGAGCCCTCGCTCTCTGAGAAC 2523

QY 779 LeuArgLeuAspCysCysGlyLeuThrHisAlaCysTyrLeuLysIleSerGlnIleLeu 798  
 Db 2524 CTGCGG----- 2529  
 QY 799 ThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLysValThrAspGlnGly 818  
 Db 2530 -----TTGGCTGGC----- 2538  
 QY 819 ValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeuGlnLysLeuIleLeu 838  
 Db 2538 ----- 2538  
 QY 839 GluAspCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858  
 Db 2539 -----TGTGGCTCACAGCTGAGACCTGCAAGAACTTGGCTTGGGCTGAGAGCCAAAC 2592  
 QY 859 ArgSerLeuThrHisIleuCysLeuSerAsnAsnSerLeuGlyAsnGluGlyValAlaAsnLeu 878  
 Db 2593 CAGAGC----- 2598  
 QY 879 LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898  
 Db 2598 ----- 2598  
 QY 899 HisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTyrLeu 918  
 Db 2599 -----CTG 2601  
 QY 919 ThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyValLysLeuLeuCysGlu 938  
 Db 2602 ACCGAGCTGGACCTGAGCTTCAATGTGCTCAGAGATGCTGAGCCAAACCTTTGCTCAG 2661  
 QY 939 ValMetArgGluProSerCysHisIleuGlnAspLeuGlyLeuValLysCysHisIleuThr 958  
 Db 2662 AGACTGAGACGCCAGCTGACCTCAAGCTACAGCACTGCAAGCTGTGAGCTGTGAGCTCAG 2721  
 QY 959 AlaAlaCysCysGluSerLeuSerCysValIleSerArgSerArgHisLeuLysSerLeu 978  
 Db 2722 TCTGACTGTGCGCAGAGACCTGGCTGTGTATGTGTCAGCCCAAGCTGAAAGAGCTA 2781  
 QY 979 AspLeuThrAspAsnAlaLeuGlyLysArgGlyValAlaAlaAlaLeuCysGluGluLys 998  
 Db 2782 GACCTGAGAGCAACAACCTGATGACGTTGGCTGTGAGCTGTGTGAGGGGCTCAGG 2841  
 QY 999 GlnLysAsnSerValLeuThrArgLeuGlyLeuLysAlaCys-----Gly 1013  
 Db 2842 CATCTGCTCCGAAATCTCAACCTGCGGAAACCAAGTGAATGACCCCTAGAGGCGC 2901  
 QY 1014 LeuThrSerAspCysCysGluAlaLeuSerLeuAlaLeuSerCysAsnArg----- 1030  
 Db 2902 CTG-----GATACGGGAGAGATGATGATATGACATCTCACTCAAGCGGAGAGATC 2955  
 QY 1031 -----HisLeuThrSerLeuAsnLeu----- 1037  
 Db 2956 GAGTCAGAGAGCGGCTCTCCAGTGTGCTCAGGCTATATCTCAAACTCTCGAGCTGAGC 3015  
 QY 1038 -----ValGlnAsnAspPheSerProLysGlyMet-----MetLys 1049  
 Db 3016 AAGATCTTCCCAATGTGCTGATGTGCAGAGAAAGCTCCCAAGAGGTAGTACCGTGGAA 3075  
 QY 1050 Leu-CysSerAlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTyrLysTr 1069  
 Db 3076 CTCTGTGCGTGCCTTCTCTGCTCTCAAGGGGACCTGATACGAAAGCTTTGG----- 3130  
 QY 1069 pGlnTyrProValGlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgVal 1089  
 Db 3130 ----- 3130  
 QY 1089 IValIleAspGlySerTrpHisSerPheAspGluAspAspArgHisLysIleGlyLeuThr 1109  
 Db 3131 -----GGAATGAC 3138  
 QY 1109 rPheArgLeuProGluSerArgAlaTrpProCysAlaLeuLeuTyrGlyMetAsnProGly 1129

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Db      3139 GATGACTTTGGGGCCCCCAGGGG-----CTGTGGCTACTGAGTACTT 3183
Qy      1129 uGlnLysLeuValSerLeuLeuAlaGlyAspPheLysSerSerThrArgPheAlaLys 1149
Db      3184 GACAAAGAAAAG-----ACTGTGACCGAGTTCAC-- 3214
Qy      1149 sSerLeuCyLeuAlaThrAlaAsnGlyLysSerGlnArgValAspAsnVal-GluGlns 1169
Db      3215 -TCCCTGAGCTGCTCTCTACCCGCTGGCCACACA--CGGGCTCTGCTTGTGTATGAGA 3270
Qy      1169 eSerProGlnPheMetAlaGlyThrGlnHisLysGlnAspLysMetLeuSerValGly- 1188
Db      3271 GAAACGGGAC-----CGTGAATGATTAATTCGTGTGTGGAC 3309
Qy      1189 --TyrSerGlyAlaTrpSerGlnThrAlaGluLeuGlyLysGlySerAsnSerAla 1208
Db      3310 CAGTTCCTGGGTGAGATCAACCCACAGCAGCTGATGTGT--GGCAGGGCTCTGCTG 3366
Qy      1208 sPheAspHisGlyLysMetAlaTrpSerLeuGlyArgGluLeuSerSerArgGlyLeu 1228
Db      3367 GACATCAA-----GGCTGAGCTGGAGCTGTGA--AGCTGTACCTCCCTCACTT 3417
Qy      1228 YS-----ProThrValLeuMetThrThrAlaValCysProGlyHisTrpGluArgLeu 1246
Db      3418 GTGGCTCTCCAAAGGG--GCCATGTGACACATCCTGT--TCCAAATGGCCCACTTTAA 3473
Qy      1246 LysSerArgGly-----TrpCysLeuAsnSerAlaAspAspHisSerGlyValSerTrpS 1264
Db      3474 AGAGAGGGGAGATGCTCTCG-----AGAAAGCAGCAGGAGGTGA 3512
Qy      1264 EF 1264
Db      3513 GC 3514

```

## RESULT 8

US-09-388-221B-11

Sequence 11, Application US/09388221B

Patent No. 6818750

GENERAL INFORMATION:

APPLICANT: Reed, John C.

TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation

FILE REFERENCE: P-IJ 3650

CURRENT APPLICATION NUMBER: US/09/388,221B

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 11

LENGTH: 4466

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(4272)

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Construct

US-09-388-221B-11

## Alignment Scores:

Pred. No.:	1,536-84	Length:	4466
Score:	948.00	Matches:	360
Percent Similarity:	38.47%	Conservative:	207
Best Local Similarity:	24.42%	Mismatches:	529
Query Match:	13.40%	Indels:	380
DB:	3	Gaps:	46

US-10-066-521-6 (1-1344) x US-09-388-221B-11 (1-4466)

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Qy      11 sErTyrgLyLeuGlnTrpCyLeuTyrgLu---LeuAspLysGlnGluInpHeGlnThrPhe 29
Db      13 GCCTGGGGCGCGCTGCTGTTACTTGAGATTCTGTGAAGAGAGAGAGAGCTGAAGAGATTTC 72

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Qy      30 LysGluLeuLeuLysLysSer---SerGluSerThrThrCysSerLeuProGlnPhe 48
Db      73 CAGCTTCTGCTCGCCAAATAAAGCGACCTCCAGAGAGCTCTTGGGTGAGAGACCCGCTCAG 132
Qy      49 GluIleGlnAlaAsnValGluCysLeuAlaLeuLeuLeuHisGlyTrpTyrgLyAla 68
Db      133 CCAGAGAAAGAGAGTGCATGAGGTGGCCCTGCTACCTGGTGGCTCAG---TATGGGAG 189
Qy      69 SerLeuAlaTrpAlaThrSerLeuSerLeuPheGlnAsnMetAsnLeuArgTrpLeuSer 88
Db      190 CAGGGGCTGGAGCTTGAACCTTCAATCTGGAGAGATGGGGCTGAGGTCACTGTGC 249
Qy      89 GluLysAlaArgAspAsp----- 94
Db      250 GCCAAGCCAGAGAGGGGAGGCAACTCTCCATTCCTTACAGCCCAAGTGAACC 309
Qy      94 ----- 94
Db      310 CACCTGGGTCTCCAGCCAAACCACTCAACCGAGTGTAAATGCCGTGATTCATGAA 369
Qy      94 ----- 94
Db      370 TTGCCGGGGGTGACCCAGGGCTCAGAGAGAAAGGTTTGAAGACAGCTGCTGACACA 429
Qy      95 -----MetLysLysSerGlnAlaMet----- 102
Db      430 TCTGAGCCCGCTGAGAGAAATCTGTGCTCAGCTCCTTCAACAGCTTCCAAAGTCC 489
Qy      102 ----- 102
Db      490 CCAAGCATGAGTCTCAAGCCAGAGATCAACCAAGCCCAATCCACAGCAGTGTCTG 549
Qy      103 -----GluGlnGluGlyAla--- 107
Db      550 GGGAGCTGGAGATCCCACTCAAGCCAGCTTACCAACCAAGAGAGGCTCTGGG 609
Qy      108 -----ThrAlaAlaGluThrGluGlu 114
Db      610 ACCCAATGCCCTCTGAGTGAAGACGTCAAGAAATTTACTACAGAAATCAGAAAGAGAG 669
Qy      115 GlnGluLysSerGlnAlaMetGlnGlnGluGlyAlaThrAlaAlaGluThrGluGlnGlu 134
Db      670 AGAGAGAAATCAGAGAAAGAGAGAGGCCCATGAGGAGGGTGTGAGAAAGCCCCCAAG 729
Qy      135 GlyHisGlyGly----- 138
Db      730 GGGCAGACAGCTTACAGCCCAACCAAGCCATGGAGCCTTCTGTGAGAGAGAGCCTC 789
Qy      139 ---AspThrTrpAspLysSerHisValMetThr---LysPhe----- 151
Db      790 TGTTCACATGCGCTCGAATAAATGAGATTTTAAACCAAAATTCACACAGCTGTACTT 849
Qy      152 -----AlaGluGluGluAspValArgArgSerPheGluAsnThr 164
Db      850 CTACAAAGACTCACCCAGAAAGCAAGATCCCTGTCAAGAGAGC----- 897
Qy      165 AlaAlaAspTrpPro-----GluMetGlnThr 173
Db      898 -----TGGCTGATTAATGTGAGAGAGATTCAGAGCATTTAATTGAGATCGAGAGC 948
Qy      174 LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValValLeu 192
Db      949 TTAATTGGCCAGGCGCTGTGATCCAA-----GAACCTCGCATGATCTACTAG 996
Qy      193 HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgArgIleValLeuCyTrpAla 212
Db      997 CAGGGGCTGCTGGAATGGAGATCAACACTGGCCAGGCGAGTGAAGAGAGAGAGAGAG 1056
Qy      213 GlnGlyGlyLeuTyrgLysGlnGlyMetPheSerTrpValPhePheLeuProValArgGluMet 232
Db      1057 AGAGCCAGCTGTATAGGGAGACCGCTTCAAGATGCTTCTTACTTCAAGCTGCAAGAGCTG 1116
Qy      233 GlnArgLysLysGluSerSerValThrGluPheLysSerArgGluTrpProAspSerGln 252

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Db	1117	GCACAGTCGCAAGCTGGTAGAGTCTGCTGAGCTCATCGGAAAAAGATGGGACAGCCATCCG	1176
Qy	253	AlaProValThrGluIleMetSerArgProGluValGlyLeuPheIleAspGlyPhe	272
Db	1177	GCTCCCATTAACAGATCTGTCTAGGCGACAGGGGGCTCTTCATCTCGATGGGTGTA	1236
Qy	273	AspArgLeuGlySerValLeuAsn---AspThrValLeuGlyValAspTrpAlaGlu	291
Db	1237	GATGAGCCAGGATGGGTCTTTCAGGAGCCGAGTTCGTGAGCTCTGTCTGACCTGAGCCAG	1296
Qy	292	LyseGlnProProPheThrLeuIleArgSerLeuMetGlyValLeuLeuProGlnSer	311
Db	1297	CCACAGCCGGCGAGATGCACTGTGTGGGCAAGTTTGGCGGAAATATCTTCCGAGGCA	1356
Qy	312	PheLeuIleValThrValArgValAspValGlyThrGlyValLeuYserGluValValSer	331
Db	1357	TCTCTTCGTGATCAGCGCTGCGGACCCAGACTGTGCAAGCTCATTCCTTCTTGGAGAG	1416
Qy	332	ProArgTyrLeuLeuValArgGlyTyrLeSerGlyGlnArgGlyLeuLeuLeuGlu	351
Db	1417	GCACGTTGGGTAAAGAGTCTCGGGGTCTCTGAGTCCACAGAGAAAGATATTTCTACAGA	1476
Qy	352	ArgGlyIleGlyGlnHisGlnIlyeThrGlnGlyLeuArgAlaIleMetAspAsnArgGlu	371
Db	1477	TATTTCAAGATGAAGGCAAGGCAAGATTAAGGCTTTAGTGTGGTAATCAACAAAGAG	1536
Qy	372	LeuLeuAspGlnGlyGlnValProAlaValGlySerLeuIleGlyValAlaLeuGlnLeu	391
Db	1537	CTCTGGGGCCCTGTGTCTTGTCCCTGGGTTGTCTGGCTGGCTGACCTGACTATGGAG	1596
Qy	392	GlnAspValValGlyIlySerValAlaProPheAsnGlnThrLeuThrGly-----Leu	409
Db	1597	CAGATGAAGCGGAAGGAAATACTCAGTCACTTCAAGACACACCAACCTCTGTCTTA	1656
Qy	410	HisAlaIleAspValPheHisGlnLeuThrProArgGlyValValArgArgGlyLeuAsn	429
Db	1657	CATTACCTTGGCCAGGCTCTCCAGACTCAGCCATTGGGA-----	1695
Qy	430	LeuGlnGluArgValValLeuIlyAspArgPheGlyAspArgMetAlaValGlnGlyValTrpAsn	449
Db	1696	-----CCCCAGCTAGAGAACTCTGTCTCTGGCTCTGGCTGAGGGCATCTGGCA	1743
Qy	450	ArgIlySerValPheAspGlyAspArgLeuMetValGlnGlyLeuGlyIlySerGlyLeu	469
Db	1744	AAAAAGACCTTTTCACTGATGACCTCAGAGACGATGGGTATGATGGGGCATCATC	1803
Qy	470	ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisGlyGlu	485
Db	1804	TCCACCTTCTTGAGATGGGTATTTTCAAGAGCACCCATCCCTGAGC-----	1854
Qy	486	GluTyrTyrThrPhePheHisIleuSerLeuGlnAspPheGlyAlaIleTyrTyrVal	505
Db	1855	-----TAGAGTTATTCACCTCTGTTTCCAGAGTCTTTTGGACGATGCTCATGTC	1908
Qy	506	LeuGlnGlyLeuGlu-----IleGluProAlaLeuGlyProLeuTyrValGluIlyThr	523
Db	1909	TTGGAGGATGAGAGAGGAGGAGTAACATTTATATGATCATCATGATTTGGAAAAAGCG	1968
Qy	524	LybArgSerMetGluLeuIlyGlnAlaGlyPheHisIleHisSerLeuTrp-----	540
Db	1969	CTAGAGACA-----TATGGAATACATGGCTTTTGGGGCATCA	2007
Qy	541	MetIlyAspPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluValLeu	560
Db	2008	ACCACAGCTTTCTATTTGGGCTGTTAAGTATGAGGGGAGAGAGAGATGGAGAAATC	2067
Qy	561	LeuGlyGlyProValProLeuGlyValIlyGlnIlyLeuLeuHisTrpValSerLeuLeu	580
Db	2068	TTTCACTGCGCGGTCTTCAGGG-----AGAACCTGATGACATGGGTCCCGTCCGTG	2121
Qy	581	Gly-----GlnGlnProAsnAlaThrThrProGlyAspThrLeuAspAlaPheHisGly	598

Db	2122	CAGCGTGGCTGCGAGCCACAC-----	-----TGTCTGAGATCCCTTCCACTGC	2163
Qy	599	LeuPhegluThrglnAspIysGlnPheValArgLeuAlaLeuAsnSerPhegluGluVal	618	
Db	2164	TTGGATACGAGATCGGACCAAAACCTTCTTGCACAAAGTAGAGGCCATTTCGAGAAATG	2223	
Qy	619	TrpIeuProIleanglnAsnLeuAspLeuIleAlaSerSerPheCysVleuGlnHisCys	638	
Db	2224	GGCATGTGTGTAGAAACAGACATGAGGTCTTAACTGTGCATCTTCTGCATTAAATTGACG	2283	
Qy	639	ProTyrLeuAlaGlySileArgValAspValLysGlyIlePheProAlaAspGluSerAla	658	
Db	2284	CGCCACGCGAAGAAAGCTTCAAGCTG---ATTGAGGGC-----AGGACACACAGATCA	2331	
Qy	659	GluAlaCysProValValProleuTrpMetArgAspIysThrLeuIleGluIuGlnTrp	678	
Db	2332	ACATGAGAGCCCGACCATAGTATGCTCTGTTCAGTGGAGGTCCCGACACAGAGCTAAATGG	2391	
Qy	679	GluAspPheCysSerMetLeuGlyThrHisProHisVleuArgGlnLeuAspLeuGlySer	698	
Db	2391	-----	2391	
Qy	699	SerIleLeuThrglnArgAlaMetLysThrLeuCysAlaIysVleuArgHisProThrCys	718	
Db	2391	-----	2391	
Qy	719	LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValGlnHisLeuTrp	738	
Db	2392	-----CAGATTCTCTTC-----	2403	
Qy	739	ArgIleValMetAlaAsnIleAspIleuArgSerLeuAsnLeuGlyIuThrHisVleuLys	758	
Db	2404	TCCGCTCTCCAGGTGCACCAAGAACTGGAAGAGCTGAGCTTAAGTGAATCTCGTGAAGC	2463	
Qy	759	GluGluAspValArgMetAlaCysGluAlaLeuIysHisProLysCysVleuLeuGluSer	778	
Db	2464	CACCTGTGAGTGAAGAGAGCTTTGTGAAGACCTTGAGACGCGCTCGCTGCTGAGAACCC	2523	
Qy	779	LeuArgLeuAspCysCysGlyLeuThrHisValaCysTyrLeuIysVleSerGlnIleLeu	798	
Db	2524	CTGGCGGTGGCTGGCTGTGAGCTGCACAGCTGAGACGTGCAGAGACCTTGGCTGGGCTG	2583	
Qy	799	ThrThrSerProSerIleuLysSerLeuSerIleuAlaGluAsnIysValThrAspGlnGly	818	
Db	2584	AGAAGCCAAACAGACCCCTTACCGAGCTGACCTGACCTTCAATGTGCTGACAGATGCTGA	2643	
Qy	819	ValMetProLysSerAspAlaLeuArgValSerGlnCysValaLeuGlnIysLeuIleu	838	
Db	2644	GCCAAACACCTTTGGCCAGAGACTAGACAGACGCCGAGCTGCAGACTACAGCACTGCACTG	2703	
Qy	839	GluAspCysGlyIleThrAlaThrGlyCysGlnSerIleuAlaSerAlaLeuValSerAsn	858	
Db	2704	GTCAGCTGTGGCTCAAGTGTGACTGCTGCACAGACCTGGCGCTCTGTAGTGCCAGC	2763	
Qy	859	ArgSerLeuThrHisVleuCysLeuSerHisAsnSerLeuGluAsnGlnGlyValAsnLeu	878	
Db	2764	CCGACGCTCGAAGAGACTGACCTGCACAGCAAACTGATGATGACGTTGGGCTGTGACTG	2823	
Qy	879	LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLysMetLeuAsnGlnCys	898	
Db	2824	CTCTGTAGAGGGCTTCAGGACTCTGCTGCTGCAAATCTACATACGCTCGGGGAAACCAAGTGTG	2883	
Qy	899	HisVleuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaLeuMetGlyAsnSerTrp---	917	
Db	2884	ATGACCCCTTACGAGGGC-----CTGGATACGGGAGAGATGAGTAAATGACATCC	2934	
Qy	918	---LeuThrHisLeuSerLeu-----SerMetAsnProValGluAspAsnGly	932	
Db	2935	TCACTCAAGCGGACAGAGATCGATACAGAGAGCGCGCTTCCCAATGTGTCTACAGCTAAT	2994	
Qy	933	ValIysVleuLeu-----CysGluValMetArgGluProSer	944	
Db	2995	CTCAAACTCTCGAGAGTGAAGATCTTCCCAATGTGTGATGATGACAGAGAAAGCTCC	3054	



Qy	108	-----ThrAlaAlaGluThrGluGlu	114
Db	610	ACCCATAGCGCTCTGGATGAACCTCAGAAATTATCTACAGAAATTCAGAAAGAGAG	669
Qy	115	GInGluIleSerGlnAlaMetGluGlnGluValAlaThrAlaAlaGluThrGluGluGln	134
Db	670	AGAGAGAAATCAGAGAAAGCAGAGGCCCATAGGCGAGCGGTGATAGAGAGCCCCCAG	729
Qy	135	GlyHisGlyIly-----	138
Db	730	GCGGACACACAGCTACAGCCCCACACCCATGGAGCCTTCTGTGAGAGAGAGCCTC	789
Qy	139	---AspThrTrpAspIlyLeuSerHisValMetThr---LysPhe-----	151
Db	790	TGTTTCATAGCGCCTGTGGAAAATAGAGATTTTATCAAAAATTTCAACAGCTGACTT	849
Qy	152	-----AlaGluGluGluAspValArgArgSerPheGluAsnThr	164
Db	850	CTACAAAGACCTCACCCCGAAGGCACAAATCCCTCGTCAAGAGAGC-----	897
Qy	165	AlaAlaAspTrpPro-----GluMetGlnThr	173
Db	898	-----TGCGCTGATTATGTGGAGAGATCGAGACATTTAATTGAGATCAGAGAC	948
Qy	174	LeuAlaGly---AlaPheAspSerAspArgTrpGlyPheArgProArgThrValIleu	192
Db	949	TTATTTGGCCCAAGCGCTGATACCAA-----GAACCTCGGATGTCTACTGCT	996
Qy	193	HisGlyLysSerGlyIleGlyLysSerAlaLeuAlaArgAlaValIleuCysTrpAla	212
Db	997	CAGGGCGGCTGCTGGAAATTGGGAAGTCAACACTGGCGAGGAGGAAGAGCCTGGGG	1056
Qy	213	GInGlyIleLeuIlyTrpGlnGlyMetCysSerTrpValPhePheLeuProValArgGluMet	232
Db	1057	AGAGGCCAGCTGTATGGGAGACCGCTTCAGAGCATGCTTCTACTTCAGCTGACAGAGCTG	1116
Qy	233	GlnArgLysLysGluSerSerValThrGluPheIleSerArgGluTrpProAspSerGln	252
Db	1117	GCCCACTCAAGGTGGTAGTGTCTCTAGCTCATCGAAAAGATGGACAGCAGCTCG	1176
Qy	253	AlaProValThrGluIleMetSerArgProGluArgLeuPheIleAspGlyPhe	272
Db	1177	GCTCCCATAGACAGATCTGCTCTAGGACAGAGGGCGCTCTTATCTGATGAGGTGTA	1236
Qy	273	AspAspLysGlySerValLeuAsnAsn---AspThrLysCysLysAspTrpAlaGlu	291
Db	1237	GATGAGCAGAGATGGGTCTTGCAGAGGCCAGATTCTGACTGTCTGCTGCATGAGCAG	1296
Qy	292	LysGlnProProPheThrLeuIleArgSerIleuArgLysValLeuIleuProGlnSer	311
Db	1297	CCACAGCCGGGAGATGCACTGTGTGGGCAAGTTTGGGGGAAATATCTTCCGAGGCA	1356
Qy	312	PheLeuIleValThrValArgAspValGlyThrGlyLysLeuLysSerGluValIleSer	331
Db	1357	TGCTTCTCGATGCAAGCGCTCGGACACACAGCTGCGAAGACTATTCCTTCTTGGAGAG	1416
Qy	332	ProArgTrpLeuLeuValArgGlyLysSerGlyGlnArgGluIleHisLeuLeuLeuGln	351
Db	1417	GCACGTTGGGTAGAGGTCTGTGGGTCTCTGAGTCCAGACAGAGAGAAATATTTCTACAGA	1476
Qy	352	ArgGlyIleGlyGlnHisGlnLysThrGlnGlyArgAlaIleMetAsnAspArgGlu	371
Db	1477	TATTTCAAGATGAAGGAGGCAATTAGAGCCTTTAGGTGTGGTAAATCAACAAAGAG	1536
Qy	372	LeuLeuAspGlnCysGlnValProAlaValGlySerLeuIleCysValAlaLeuGlnIleu	391
Db	1537	CTCTGGGCGCTGTGTCTTGTGGCTCGGGATGTCTGGCTGGAGCTTGGCTATGGAG	1596
Qy	392	GlnAspValAlaGlyLysSerValAlaProPheAsnGlnThrLeuThrGly-----Leu	409
Db	1597	CAGATGAAGCGGAGGAAAACTCACACTGACTTCAAGACCCACACAAACCTCTGTGCTA	1656

QY	410	HisIaIaIaPheValPheHisIGLLeuThrProArgGlyValValAArgGlyLeuLysN	429
Db	1657	CAITTAACCTTGCCCAAGCTCTCCAGACCTCAAGCCATTGGGA-----	1693
QY	430	LeuGIuGIuAArgValIaLeuLysArgPheCysArgMetAlaValGIuGIyValTrrpAsn	449
Db	1696	-----CCCCAGCTCAGAGACCTCTGGCTCTGGCTGGCTGAGGGCATCTGGCA	1744
QY	450	ArgIysSerValPheAspGlyAspAspLeuMetValGInGIyLeuGIyGluSerLysLeu	469
Db	1744	AAAAAGACCTTTTTCAGTCCAGATGACTCCAGAAAGCATGGATTGATGGGCCATCATC	1801
QY	470	ArgAlaLeuPheHisMetAsnIleLeu-----LeuProAspSerHisCysGluN	485
Db	1804	TCCACCTCTTGAAGATGGGATATCTTCAAGAGCAACCCCATCCCTGAGC-----	185
QY	486	GluTyrTyrThrPhePheHisLeuSerLeuGlnAspPheCysValAlaLeuTyrTyrVal	505
Db	1855	-----TACACCTTCATTCACCTCTGTTTCCAAAGATCTTTGGACGAATGCTCTAATGC	1900
QY	506	LeuGIuGIyLeuGluN-----IleGluProAlaLeuCysProLeuTyrValGIuTyrThr	523
Db	1909	TTGGAGATGAGAAAGGAGAGATTAACATTTCTAATTCATCATGATTTGGAAAAAGAC	1966
QY	524	LysArgSerMetGluLeuLysGlnAlaGlyPheHisIleHisSerLeuTrrp-----	540
Db	1969	CTAGAAGCA-----TATGAAATACATGCGCTGTTTGGGCATCA	2007
QY	541	MetyIaArgPheLeuPheGlyLeuValSerGIuAspValAArgPProLeuGIuValLeu	560
Db	2008	ACCACACCTTTCATATGGCGCTGTTTAATGATGAGGGGAGAGAGATGGAGAAACATC	2066
QY	561	LeuGIyCysProValProLeuGIyValLysGlnLysLeuLeuHisTrrpValSerLeuLeu	580
Db	2068	TTTCACTCCCGGCTGCTCAAGGG-----AGAACTGTCGACATGGGTCCGTCCTG	2122
QY	581	Gly-----GInGlnProAsnAlaThrThrProGIyAspThrLeuAspAlaPheHisCys	598
Db	2122	CAGCTGCTGTCGACCAACAC-----TCTCTGAAGTCCCTTCACATGC	2166
QY	599	LeuPheGIuThrGlnAspLysGluPheValArgLeuAlaLeuAsnSerPheGInGIuVal	618
Db	2164	TTGTACGAGATCTCGGAACAAACGTTCTTGACACAAAGATGGCCCATTTGCAGAAATAG	2222
QY	619	TrrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys	638
Db	2224	GGCATGTGTGAGAAACAGACATGAGGCTCTTAAGTGCACATTTCTGCATTAAATCAGC	2283
QY	639	ProTyrLeuAlaGlyLysIleArgValAspValLysGlyIlePheProArgAspLysSerIa	658
Db	2284	CGCCACGTGAAGAACCTTCAGTGT--ATTGAGGC-----AGGACAGCAAGATCA	2333
QY	659	GluAlaCysProValValProLeuTrrpMetArgAspLysThrLeuIleGluGIuGIuTrrp	678
Db	2332	ACATGAGACCCCAACATGATGATGCTCTGTCAGTGGGTGCCAGTGCACAGATGCTTAATGG	239
QY	679	GluAspPheCysSerMetLeuGIyThrHisIProHisIleuArgGlnLeuAspLeuGIySer	698
Db	2391	-----	239
QY	699	SerIleLeuThrGluArgAlaMetLysThrLeuCysValAlaLysArgHisIProThrCys	718
Db	2391	-----	239
QY	719	LysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGIyValGlnHisIleuTrrp	738
Db	2392	-----CAGATTCTCTTC	240
QY	739	ArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGIyGIyThrHisIleuLys	758
Db	2404	TCCGCTTCACAGTCAACCAAGAACTGGAAGAGCTGAGACCTTAAGTGAAGAACTCGCTGAC	2466
QY	759	GIuGIuAspValAArgMetAlaCysGIuAlaLeuLysHisIProLysCysIleuLeuGIuSer	778



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Db      2464 CACTGTGAGTGAAGAGCTTTGTAAGACCTGAGAGACCTCGCTGCTCTGAGAGACC 2523
Qy      779  LeuArgLeuArgCysGlyLeuThrHisAlaCysIleLeuValIleSerGlnIleLeu 798
Db      2524 CTGGGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 2583
Qy      799  ThrThrSerProSerLeuLeuSerLeuSerLeuValIleLeuValIleLeuValIleLeu 818
Db      2584 AGAGCCACCAAGACCTGAGACCTGAGACCTGAGACCTGAGACCTGAGACCTGAGACCTGAG 2643
Qy      819  ValMetProLeuSerAspAlaLeuArgValSerGlnValAlaLeuGlnIleLeuIleLeu 838
Db      2644 GCCAAACCTTTGCGAGAGCTGAGACAGCCGAGCTGCAAGCTTACAGCACTGAGCTG 2703
Qy      839  GluArgCysGlyIleThrAlaThrGlyCysGlnSerLeuAlaSerAlaLeuValSerAsn 858
Db      2704 GTGAGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2763
Qy      859  ArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuGlnValAsnGlnValAlaAsnLeu 878
Db      2764 CCCAGCTGAAAGAGCTTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2823
Qy      879  LeuCysArgSerMetArgLeuProHisCysSerLeuGlnArgLeuMetLeuAsnGlnCys 898
Db      2824 CTCTGTGAGGGGCTCAGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2883
Qy      899  HisLeuAsp----- 901
Db      2884 ACTGTGAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2943
Qy      902  -----ThrAlaGlyCysGlyPheLeu 908
Db      2944 CTCAATCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2994
Qy      909  AlaLeuAlaLeuMetGlyAsnSerTrp-----LeuThrHisLeuSerLeu----- 923
Db      2995 GATACGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3054
Qy      924  --SerMetAsnProValGluAspAsnGlyValIleValLeu----- 936
Db      3055 AGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3114
Qy      937  -----CysGlnValMetArgGluProSerCysHisLeuGlnAspLeuGlnValIle 954
Db      3115 CCAATTGCTGAGATTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3174
Qy      954  sCys-----HisLeuThrAlaAlaCysCysGlnSerLeuSerCysValIleSerArg 971
Db      3175 GTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3234
Qy      971  gSerArgHisLeuLeuValSerLeuAspLeu-----ThrAspAs 983
Db      3235 TTTCGTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3294
Qy      983  nAlaLeuGlnValAspGlyValAlaAlaLeuValLeu----- 995
Db      3295 AGCGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3354
Qy      996  -----GlyLeuValSerGlnValAsnSerValLeuThrArgGlnGlyLeuValAlaCysGlyLe 1014
Db      3355 GTAAGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 3414
Qy      1014  uThrSerArgCysCysGlnAlaLeuSerLeuAlaLeuSerCysAsnArgHisLeuThrSe 1034
Db      3415 GACCTGCAAGACCATGAAACAGTGGCTGTGGGCGGCCCTTTGTGATGATCACTCAAGAG 3474
Qy      1034  rLeuAsnLeuValGlnAsnAsnPheSerProGlyGlyMetMetCysLeuCysSer----- 1052
Db      3475 C-----CAGAGAGAGCTGTGCGCGAATTCACACTTCCCTTCCCTC 3522
Qy      1053  -----AlaPheAlaCysProThrSerAsnLeuGlnIleIleGlyLeu-----TrpIly 1068

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Db      3523 CAGGTGAGTGAAGCTCTCGGTGTTCTCGTCCCATTTTAAAGATGAAGGATGCTC 3582
Qy      1068 sTrpGlnTrpProValGlnIleArgGlyLeuLeuGlnGlnValGlnIleLeuValProArg 1088
Db      3583 CTGAGG-CATCAGACCCGGGGTGAAGCTTTTATAGTCTCTCTGAAA-----AGCCCAAG 3635
Qy      1088 gValValIleAspGlySerTrpHisSerPheAspGlnAspAspArgHisIleValLe 1108
Db      3636 CTTCCTCTGANTGGGCAATCCGTGGGATGCGGAGTGGAGAGTGGAGCTGCTCATTCCTCAT 3695
Qy      1108 uThrPheArgLeuProGlnSerArgAlaTrpProCysAlaLeuLeuTrpGlyMetAsnPr 1128
Db      3696 CACTTCCAAAC-----ACATGTATCTATATATCAACCCCACTC 3731
Qy      1128 oGlnGln---LysIleArgValSerLeuLeuAlaGlyAspPheLeuSerSerThrArgPh 1147
Db      3732 GAAAGATATTAAGTTTCCACTGTATCTGTCTCCAGCAAC----- 3771
Qy      1147 eAlaLeuSerLeuCysLeuAlaThrAlaAsnGlyGlnSerGlnArgValAspAsnValGln 1167
Db      3772 -----GCTTGTCTAACAAGGCGATGATGATGATGATGATGATGATGATGATGATGATG 3824
Qy      1167 uGlnSerSerProGlnProMetAla-----GlyThrGlnHis----- 1179
Db      3825 CTGCAAGCTTCGCCCCCAATGGAACCCCTGAAGCTTGTGCTTCCAGTTATATGTGTCTAA 3884
Qy      1180 -----LysGlnAspIleMet----- 1184
Db      3885 TTTCCTAATCTGAAAGATATGCCCAAGAGATGAAATTTGCTTACAGAGACCTCGAGA 3944
Qy      1185 -----LeuSerValGlyTrpSerGlyAlaTrpSerGlnThrAlaGlnLeuGlnGln 1201
Db      3945 AATTACAGACTTCTCAAAATTTCTATGCTGGGAGATGAAGAGAACCATTTCAACTGAG-- 4002
Qy      1201 yLeuGlySerAsnSerAlaAspHisAspHisGlyGlyMetAlaTrpSerLeuGlyArgGln 1221
Db      4003 -----ATTACTGAAAAAAGACATGGACTTGTGTGGGATPACTGA-GGTGA 4048
Qy      1221 uLeuSerSerArgGlyLeuCys-----ProThrValLeuMetThrThrAlaVal 1237
Db      4049 AGCCAGTGAATCTCCAGCTTGTAGCTGCATGACGCCCTTCCTCTTCTCAGGTGAGCCT 4108
Qy      1237 lCysProGly 1240
Db      4109 TTGTGAAGGA 4118

RESULT 10
US-10-183-770A-1
; Sequence 1, Application US/10183770A
; Patent No. 6949363
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED
; FILE REFERENCE: D0067A CIP
; CURRENT APPLICATION NUMBER: US/10/183,770A
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US 60/257,773
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 10/028,374
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4931
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1320)..(2666)
US-10-183-770A-1
Alignment Scores:

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Db      2520 GCCTACAGTGAACATCTGGACGGCCCTGTGGACCAATCCAACTGATAGAGTGTCT
Qy      696 LeuGlySerSerIleuThrGluArgAlaMetCysThrLeuCyValAlaLeuArgHis
Db      2580 CTGTACCGAATATGCTGGGACGGCGGGGTGAAGCTGCTCTGTCAAGAGCTCAAGAAC
Qy      716 ProThrCysValIleGlnThrLeuMetPheArgAsnIleGlnIleThrProGlyValGln
Db      2640 CCCAACTGCACAACTTCAGAACCTTAGAGTAAATTTATCATATATACATGATATTTTGA
Qy      736 ---HisLeu---TyrArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGly
Db      2700 ATAATATATATTGGCAGGTATAGATGGCTCAGGCC---TGTAAATCCAGACCTTTGGAGG
Qy      754 Y-----ThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLys
Db      2757 CCCAGATGGGAGGATCATTGACCCAGAGATTCAAGACCAAGCTTGCCAAATGGTGA
Qy      770 HisProLysCysLeuLeuGluSerLeuArgLeuAspCysCysGlyLeuThrHisAlaCys
Db      2817 ACC-CCATCTCTACTAA-ATAAC-----
Qy      790 sTyLeuLysIleSerGlnIle-----LeuThrThrSerProSerLeuLysSerIle
Db      2840 -----AAATATGACCCAGGACATGGTGGACACAGCTGTATAGCCCAAGCTACTCAGAGAGC
Qy      807 uSerLeuAlaGlyAsnLysValThrAspGlnGlyValMetProLeuSerAspAlaLeuArg
Db      2893 CAAGCAGAGAGG-----
Qy      827 gValSerGlnCysAlaLeuGlnLysLeuLysLeuGluAspCysGlyIleIleThrAlaThrGly
Db      2906 -TTCTCTTAACCCAGAGCAGAGAGGTGTGGCTGAAGAGGTGCCAGCTATCCAGTCCAGC
Qy      847 YCysGlnSerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSe
Db      2965 CTGGAGAGACCTCTCTGACGCTCTCATAGCCAAATTAATTTGACAAGATGAGATCTCAG
Qy      867 rAsnAsnSerLeuGluLysAsnGluGlyValAsnLeuLeuCysArgSerMetAlaGluProHis
Db      3025 TGGGCAACGCGCTTGATTCACAGGAGATGATGCTGTTGGCAGAGGCTGGCGGCAATCCCA
Qy      887 sCysSerLeuGlnArgLeuMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPhe
Db      3085 ATGCAAGCTGCAAGATTCAGTTGAGAGAGTGAAGTCCGGGGCTGTTCAGAGA
Qy      907 eLeuAlaLeuAlaLeuMetGlyAsnSerTyrLeuThrHisLeuSerLeuSerMetAsnPr
Db      3145 GATGGCTTCTGTGCTTGGACACCAACCAATCTGTGATTTGACCTGACAGAGAAATGC
Qy      927 oValGluAspAsnGluValLysLeuLeuCysGluValMetArgGluProSerCysHisLe
Db      3205 ACTGAGAGATTTGGGCTGAGAGGTACTATGCCAGAGGACTGAGAGGCCACCAAGTCTGAGACT
Qy      947 uGluAspLeuGluLeuValLysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCys
Db      3265 ACGGACTTTGGCTGGAAGATCTCCGCTCACTCTGCTGCTGTGACAGACTGGCTTC
Qy      967 sValIleSerArgSerArgHisLeuLysSerLeuAspLeuThrAspAlaAlaLeuGlyAs
Db      3325 AACTCTCAGTGTGAACCAAGAGCTGAGAGAGTGAAGTCAAGCTGAGAGTGGGGA
Qy      987 pGlyValValAlaAlaLeuCysGluGlyLeuLysGlnLysAsnSerValLeuThrArgLe
Db      3385 CCTGGGGGTGCTGCTGTGTGAGGGCTCAGGATCCCAAGTCAAGCTTCAGACCT
Qy      1007 U-----GlyLeuLysAlaCysGlyLe
Db      3445 GCGGTAGTCCCGTTTGTCTCAACAGCTAGAGTCCCAATCATCAAGAGCA---GCCCT
Qy      1014 uThrSerAspCysCysGluAla---LeuSerLeuAlaLeuSerCysAsnArgHisLeuThr

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Db      3502 CTCACTGGGACCAAGAGGCCAGTTGTCTGTGCTCTTAACCTAGTACTACATCAG
Qy      1033 rSer-----
Db      3562 CCTTTTATTTTTTTTTTTTGGAGACTCCCAAGTACGTAGATTAAGGCCGCCGCCACCA
Qy      1035 -----LeuAsnLeuValGlnAsnAspHe-----SerProLysGly
Db      3622 GCCAGGTAATTTTGTATATTTAGTAGAGACAGGGTTTCATCATGTATGACAG-GATGG
Qy      1046 yMetCysLeuLeuCysSerAlaPheAlaCysProThrSerAsnLeuGlnIleGlyLe
Db      3681 TCTGATCTACTGACCTTCATGATCTGCTGC-----
Qy      1066 uTyrLys---TyrGlnTyrProValGlnIleArgLysLeuLeuGluValGlnLeuLe
Db      3720 CCCAAAGTCTGGGATTAAC-----AGCTTGAGCCACTGACCCAGCTTACATCAGCT
Qy      1085 uLysProArgValAlaIleAspGlySerTyrHisSerPheAspGluAspArgHisLys
Db      3774 TTTTAAAGATTTTTCGCGCGG-----CATGGTGGCTGACACCT
Qy      1105 sIleGlyLeuThrPheArgLeuProGluSerArgAlaTyrProCysAlaLeuLeuTyrGly
Db      3816 TAATTCAGCACTTTTGGAGGCCGAG-----TGGAGAGATCACTCAGAGTGGG
Qy      1125 yMet-----AsnProGluGlnLysLysArgValSerLeuLeuAlaGlyAspPheLysE
Db      3867 AATTCGAGACCAAGCTTACCAATGTAAGAAACCCCATTTGATCTAATAATTCAAAG
Qy      1143 rSerThrArgPheAlaLysSerLeuCysLeuAlaThrAlaAsnGlyLeuSerGlnArgVal
Db      3927 TAGCCAGGCAATG---TGTGCATGCTCATTAATGACAGTACTGCGAGGCTGAGGACAG
Qy      1163 lAspAsnValGluGlnSerSerProGlnProMetAlaGlyThrGluHisLysGlnAspLys
Db      3984 AGAATCCGTTGA-----
Qy      1183 sMetLeuSerValGlyTyrSerGlyAlaTyrSerGlyLys---AlaGluLeuGlnGlyLe
Db      3997 -----CCGGAGGTGGAAGTTGCTGTGAGCTGAGATGAGCCATT
Qy      1202 uGlySerAsn-----SerAlaAspHisAspHisGlyLys
Db      4038 GCACCTCAGCTGGGCAACAGAGGAACTCCGCTCAAAAAAAGAGGGGGGCTT
Qy      1214 cAlaTyrSerLeuGluArgLysLeuSerSerArgGlyLeuCysProThr-----
Db      4098 TTCT-----GAGGACGGCC-CTTGGCAACAGCAATTTCTTATTC
Qy      1231 -----ValLeuMetThrThrAlaValCysProGlyHisTyrGlu-----
Db      4136 CCTGGCATGCTTCTGCTGTCTGTCCTCTTTCGCTTGAAGAGTTCAAATTTTCTTCTG
Qy      1244 -----ArgLeuGlySerArgLys-----
Db      4196 AACACTCTTACTTGTATTTTGAAGACAGGCTTGTCTGTACCAAGTGTGGAGTGA
Qy      1250 -TyrCysLeuAsnSerAlaAspAspHisSerGlyValSerTyrSer
Db      4286 GTGGTGT-----GATCATAGCCCGCAATCTGGGCT

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# RESULT 11

```

US-10-781-294-17
; Sequence 17, Application US/10781294
; Patent No. 6953691
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia

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Qy 572 ysleuLeuH1sTPrVAlSerleuLeuGlyGln-----GlnProAsnLat 587
Db 1721 AGGCGCTGGGCTGAGGAGCAAGGAGGCTGCCCGAGTGGCACAGAGGTGA 1780
Qy 587 hr-----T 588
Db 1781 CCGAGGGGGGCAAAAGGCTGAGGACACCGAAGGCCAGAGAGGAGGAGGAGAGG 1840
Qy 588 hrPrGlyAspThrLeuAspAlaPheH1sCyLeuPheGlnThrGlnAspGlyPheV 608
Db 1841 AGCCCACTACCCACTGAGAGTGGCTGACTCTGCTGACAGACGAGAGCAGCGCTTGG 1900
Qy 608 AlaGlyLeuAlaLeuAsnSerPheGlnGlyValThrPheProIleAsnGln-----AsnL 626
Db 1901 TGGCCCAAGCCCTTGCGCGGTCCCGAGCTGGCGGCTGACAGAGTGGCTTTCGCCCA 1960
Qy 626 euAAspLeuIleAlaSerSerPheCyLeuGlnH1sCyProTyLeuArgHysIleArgV 646
Db 1961 TGGACGTGGCTGTTCTGAGCTACTGCTGAGAGGTGCTGCTGCTGAGAGGACCTGGCG 2020
Qy 646 AlaAspValLeuGlyIle-----PheProArgAspGlySerAlaGlyAlaAc 661
Db 2021 T-GATCAGCTCAGATTTGCTGTCGCGAGAGAAAGAAAGAGAGCTGGCGGAGCGG 2079
Qy 661 ysPrOvalValProLeuThrMetArg-----AspGlyThrLeuLeuGlnGlnT 678
Db 2080 CTCGAGGCGGACCTGGGTGGCGGCGGCTGGGAGCCCAACTGG-CTCGAAGAGTACC 2138
Qy 678 TrpGluAspPheCySerMetLeuGlyThrH1sProH1sLeuArgGlnLeuAspLeuGlyS 698
Db 2139 CTTTCGACACCCCTGCTGTGACATCTGCC---CACACCTTCCACAG---ACCTCGGCT 2192
Qy 698 erSer-----IleLeuThrGluArgAlaMetLysThrLeuCyAlaLeuLeuArgH 715
Db 2193 CCTCCAGGCGAAGGCTTTGGCCAGAG-----TTCCTTGAATATATAGCTCCCAAT 2240
Qy 715 isPrOThrCyValLeuGlnThrLeuMetPheArgAsnAlaGlnIleThrProGlyValG 735
Db 2241 TCAGCCCTGTC-----CCAGGGGCTT 2261
Qy 735 InH1sLeuTrpArgIleValMetAlaAsnArgAsnLeuAspSerLeuAsnLeuGlyI- 754
Db 2262 GGCATCTTTGAGAGAGATGATG---TCACGGTGTGGCAGGGGCTGGCGCTGGGAGC-C 2317
Qy 755 -----ThrH1sLeuArgGluLeuAspValArgMetAlaCyseGluAlaLeuLysH1sPrO 773
Db 2318 CAAGAGCCCAT-----GCAATGACTGACCCAC 2344
Qy 773 ysCyLeuLeuGlnSerLeuArgLeuAspCyseGlyLeuThrH1sAlaCyseTyLeuL 793
Db 2345 TGTGTCATCTGAGCGCTCAGCTGCTCCCACTGCAAACTCCCTGACCGGTCTGCCGAG 2404
Qy 793 ysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnL 813
Db 2405 ACCTTTCTGAGGCCCTGAGGGGAGGCCCGGCACTACGAGAGTGGGCTCTCCCAACA 2464
Qy 813 ysValThrAspGlnIlyValMetProLeuSerAspAlaLeuArgValSerGlnCyAlaAl 833
Db 2465 GGCCTCAGGAGGAGGAGCTGCGTATGAGTGAAGGAGGCTGAGCGCGAGTGCAGAGG 2524
Qy 833 euGln-----LysLeuIleLeuGluAspCyseGlyIleThrAlaThrGlyCyseGlnSerL 851
Db 2525 TGCACAGCGGTGAGGTACAGCTGCTGAC-----CCCGAGGAGGAGGCTCCCAATACC 2575
Qy 851 euAlaSerAlaLeuValSerAsnArgSerLeuThrH1sLeuCyAlaSerAsnAsnSerL 871
Db 2576 TGGTGGGTATGTTTGGCAGAGCCCTGCCCTTACACCTGATCTCAGCGGCTGCCAAC 2635
Qy 871 euGlyAsnGluGlyValAsnLeuLeuCyAlaArgSerMetArgLeuProH1sCyseSerLeuG 891
Db 2636 TGCCCGGCCCCCATGCTGACTTACTGTGTGACGCTCTGACAGACAGAGGAGTGGCGCTGC 2695

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Qy 891 InArgLeuMetLeuAsnGlnCyseH1sLeu 900
Db 2696 AGACCTTCAGTCTGCGCTGTGTGAGCTG 2724

RESULT 12
US-10-781-294-58
; Sequence 58, Application US/10781294
; Patent No. 6953691
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Chu, Zhi-Liang
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Ariza, Maria Eugenia
; APPLICANT: Stehlik, Christian
; TITLE OF INVENTION: PAD Domain-Containing Polypeptides,
; FILE REFERENCE: P-LJ 4816
; CURRENT APPLICATION NUMBER: US/10/781,294
; PRIOR APPLICATION NUMBER: US/09/965,621
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/671,760
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (176)...(2332)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (306)...(458)
; OTHER INFORMATION: n = A,T,C or G
US-10-781-294-58

Alignment Scores:
Pred. No.: 2,19e-60 Length: 2524
Score: 705.00 Matches: 178
Percent Similarity: 47.91% Conservative: 131
Best Local Similarity: 27.60% Mismatches: 250
Query Match: 9.97% Indels: 86
DB: 3 Gaps: 12

US-10-066-521-6 (1-1344) x US-10-781-294-58 (1-2524)
Qy 50 IleguAsnAlaAsnValGluCyLeuAlaLeuLeuH1sGluTyTrpGlyAlaSer 69
Db 476 GTTTCGAATCCCACTGTATATGCGAGAGACAGCATTTGAAGAGAGTGGCTTTA 535
Qy 70 LeuAlaTrpAlaThrSerIleSerIlePheGluAsnMetAsnLeuArgThrLeuSerGlu 89
Db 536 CTGAGATACCTTTGAGAAATCTTATTGTGTAATGAAG-----AAAGATTACCGTAG 589
Qy 90 LysAlaArgAspAspMetLysLysIleSerGlnAlaMetGluGlnGlnGlyAlaThrAla 109
Db 590 AAGTACAGAAAGTACGTGAGAGAGCATTCAGTGCATTGAAGACAGGAATGCCGCTCG 649
Qy 110 AlaGluThr-----GluGluGlnGlu 116
Db 650 GGTGAGAGTGTGAGCTTCAACAACGTTACACAGCACTGCGTCTCATCAAGAGCACCGG 709
Qy 117 IleserGlnAlaMetGluGlnGlnGlyAlaThrAlaAlaGluThrGluGlnGlnGlyH1s 136
Db 710 AGCAGCAGAGAGAGGAGACAGAGAGCTTGGCCATCGCAGAAC- 754
Qy 137 GlyIAspThrTrpAspTyLysSerH1sValMetThrLysPheAlaGluGluAsp 156
Db 754 ----- 754

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Qy 443 AlavaGluGluValTPrAsnArgLysSerValPheArgLysAspArgMetValGln 462
Db 112 GCTCAGAGAGAGCTGTTCTGAGCACTTGAATTTGAGTGTGAAGAGCTTGAATGTT 171
Qy 463 G1YLeuG1YLeuSerG1YLeuArgAlaLeuPheN1sMeAsnL1eLeuLeuProAspSer 482
Db 172 GGGTTTACTAGAGCTGATGCTGTGTGTGTGAGCGCGGAAATATCTTTTCCGAGCAAC 231
Qy 483 HisCysGluGluTyrTyrThrPhePheN1sLeuSerLeuGlnAspPheCysAlaAlaLeu 502
Db 232 ACTCATAAAGACCTTACAGATTCATACATTTGAACGTCGAGAGATTGTGTACAGCCATT 291
Qy 503 TyrTyrValLeuGluGluLeuGluLeuLeuProAlaLeuCysProLeu----- 518
Db 292 GCATTTCG-----ATGCAATACCCCAACTTGTGATCCCTTCAGGACGACAGAG 342
Qy 519 TyrValGluYsThrLysArgSerMetGluLeuYsGlnAlaGlyPheN1sIleHisSer 538
Db 343 TATTAAGAGAGAGAAACAATATCTGACTTATCA----- 381
Qy 539 LeuTrpMetLysArgPheLeuPheG1YLeuValSerGluAspValArgArgProLeuGlu 558
Db 382 -----GAGTTACTTTGATTTCCGCTCTTAAATGCAACAGGAGAAAGATTCTTGAG 435
Qy 559 ValLeuLeuG1YCysProValProLeuG1YValYsGlnYsLeuLeuN1sTrpValSer 578
Db 436 ACATCTTTTGATACCAAGTACCCAGTGTGACAGCTTCAAG-----TGAGTACTCG 486
Qy 579 Leu-----LeuG1YGlnInProAsnAlaThrThrProG1YAspThrLeu 593
Db 487 GTGGGATACATGAACAATTTGAGACCTGACCCGAAAGATTGAGC-----CACATATG 540
Qy 594 AspAlaPheN1sCysLeuPheGluThrGlnAspLysGluPheValArgLeuAlaLeuAsn 613
Db 541 CCTTTGTTTACTGCTCTATGAGATCGGAGAGAAATTTGTGAACGATTTGTGAT 600
Qy 614 SerPheGlnGluValTrpLeuProL1eAsnGlnAsnLeuAspLeuAlaSerSerPhe 633
Db 601 GCTCTCATGAGAGTTACAGTTTACCTTCATGCAACAAGATATGCTCTCATTAATAC 660
Qy 634 CysLeuGlnHisCysProTyrLeuArgLysIleArgValAspValYsG1YIlePhePro 653
Db 661 TGTCTGATTTACTGCTGTCACTGAGCACTTAAGTTGAGGTTCAGCGCATCTTTCAA 720
Qy 654 ArgAspGluSerAlaGluAlaCysProValValProLeuTrpMetArgAspLysThrLeu 673
Db 721 AACAAAGAG-----CCACTATA----- 738
Qy 674 IleGluGluGlnTrpGluAspPheCysSerMetLeuG1YThrN1sProH1sLeuArgGln 693
Db 738 ----- 738
Qy 694 LeuAspLeuGlySerSerIleLeuThrGluArgAlaMetLysThrLeuCysAlaLysLeu 713
Db 738 ----- 738
Qy 714 ArgHisProThrCysLysIleGlnThrLeuMetPheArgAsnAlaGlnIleThrProGly 733
Db 739 ---AGGCCAAGCTGAGGTGTGCTATGTC-----TCGAGTCTCTTCTGAT 780
Qy 734 ValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSerLeuAsnLeuGly 753
Db 781 TTTGAAGACTTATCACTCAAGCTTTGCTGTAATCGAGCTG----- 822
Qy 754 GlyThrHisLeuLysGluGluAspValArgMetAlaCysGluAlaLeuLysHisProLys 773
Db 822 ----- 822
Qy 774 CysLeuLeuGluSerLeuArgLeuAspCysCysG1YLeuThrHisAlaCysTyrLeuLys 793
Db 823 -----ACATACCTGAGT 834

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Qy 794 IleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeuAlaGlyAsnLys 813
Db 835 ATCAAC-----TGAAGTCCATTTCCCTAAATATGTTTCACTT----- 873
Qy 814 ValThrAspGlnGlyValMetProLeuSerAspAlaLeuArgValSerGlnCysAlaLeu 833
Db 874 -----CTGCATACACATCTGTGACGAGCCCAATGCCAATATA 909
Qy 834 GlnYsLeuIleLeuGluAspCysG1YIleThrAlaThrGluCysGlnSerLeuAlaSer 853
Db 910 AGTCATCTGAGCTTGATGAATGATGATTTGAGCCAGCCAGATGCGAAATAGCCCTCT 969
Qy 854 AlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsnSerLeuLysAsn 873
Db 970 CTCTCATACAGTGGCGGAGGTCTGAAGAACTGACTTATCAGCAATCCCTGAGAGAGC 1029
Qy 874 GluGlyValAsnLeuLeuCysArgSerMetArgLeuProH1sCysSerLeuGlnArgLeu 893
Db 1030 GACCGAGATGAACAATAGCTGTGATGAGCCCTGTTCATGCCAATCCATCTTATATCACTG 1089
Qy 894 MetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAlaLeuAlaMet 913
Db 1090 GTGTAGTCTTCTGTCTGATTTGAATTTGCTGAGCCCTTGGAAAGTCTTCTG 1149
Qy 914 GlyAsnSerTrpLeuThrHisLeuSerLeuSerMetAsnProValGluAspAsnGlyVal 933
Db 1150 TTCAAGCCCACTGTAAAGCAATAGCTGAGTGTGATGATGCTTAAATAATTAAGAGATG 1209
Qy 934 LysLeuLeuCysGluValMetArgGluProSerCysHisLeuGlnAspLeuGluLeuVal 953
Db 1210 TTGCATGTGAGAGTTTCCCTGCTGTTCCAACTGTGATGAGAGAGACTTCACTGTCT 1269
Qy 954 LysCysHisLeuThrAlaAlaCysCysGluSerLeuSerCysValIleSerSerArg 973
Db 1270 GAGCTGTTCTTTAGAGAGATATGTGCAATATATGTCATAGTTATTTCTACTATGA 1329
Qy 974 HisLeuLysSerLeuAspLeuThrAspAsnAlaLeuGluYsAspGlyValAlaAlaLeu 993
Db 1330 AAACGTAGAGACCTGTGAGATTTGGAGAGCAAAATAGAAAGATGAGAAATGAGCTGCTA 1389
Qy 994 CysGluGluLeuLysGlnYsAsnSerValLeuThrArgLeuGluYsLeuAlaCysGly 1013
Db 1390 TGTGCTGTGTGAGACATCCCACTGCAATGTTGTGATATATTTGGCTTGAAGAGTGCATG 1449
Qy 1014 LeuThrSerArgCysCysGluAlaLeuSerLeuAlaLeuSerCysAspArgHisLeuThr 1033
Db 1450 TTACCAAGTGCCTGTGTGATCTTGTCTGTCTTGTACCAACCAACAACTTAAGAA 1509
Qy 1034 SerLeuAsnLeuValGlnAsnAspPheSerProLysGlyMetMetLysLeuCysSerAla 1053
Db 1510 AGACTCAACTGCTTCAAAATACACTTGGCGCAATATGAGATTTGCAAAATCTTGTAGAGC 1569
Qy 1054 PheAlaCysProThrSerAsnLeuGlnIleIleGlyLeuTrpLysTrpGlnTyrProVal 1073
Db 1570 TTGATCAGCCAGATTTGTGACTTAAAGGTAGTGGCTTCAATTAATAGCTGAGCAACA 1629
Qy 1074 GlnIleArgLysLeuLeuGluGluValGlnLeuLeuLysProArgValValIleAspGly 1093
Db 1630 CAAGCCCAAGAGTGTATATATGATTAAGAAAGAAAGAAAGAAAGTGTATCTTTGTGTCT 1689
Qy 1094 SerTrpHisSerPheAspGluAspArgArgHisLysIleGlyLeuThr 1109
Db 1690 GAAACTTGCTTTTAAAGAAAGC-----AGAGAAATTTGGTGTGACA 1731

```

RESULT 14  
 US-10-781-294-19  
 ; Sequence 19, Application US/10781294  
 ; Patent No. 6953691  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, John C.  
 ; APPLICANT: Godzik, Adam  
 ; APPLICANT: Chu, Zhi-Liang  
 ; APPLICANT: Pawloweki, Krzysztof



/ APPLICANT: Fiorentino, Ioredana  
 / APPLICANT: Ariza, Maria Eugenia  
 / APPLICANT: Stehlik, Christian  
 / TITLE OF INVENTION: PAD Domain-Containing Polypeptides,  
 / TITLE OF INVENTION: Encoding Nucleic Acids, and Methods of Use  
 / FILE REFERENCE: P-1J 4816  
 / CURRENT APPLICATION NUMBER: US/10/781,294  
 / PRIOR FILING DATE: 2004-02-17  
 / PRIOR APPLICATION NUMBER: US/09/965,621  
 / PRIOR FILING DATE: 2001-09-25  
 / PRIOR APPLICATION NUMBER: US 09/671,760  
 / PRIOR FILING DATE: 2000-09-26  
 / NUMBER OF SEQ ID NOS: 64  
 / SOFTWARE: FastSeq for Windows Version 4.0  
 / SEQ ID NO 19  
 / LENGTH: 2046  
 / TYPE: DNA  
 / ORGANISM: Homo sapien  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: (1)...(2043)  
 / US-10-781-294-19

## Alignment Scores:

Pred. No.:	1,41e-54	Length:	2046
Score:	646.00	Matches:	190
Percent Similarity:	46.57%	Conservative:	122
Best Local Similarity:	28.36%	Mismatches:	294
Query Match:	9.13%	Indels:	64
DB:	3	Gaps:	13

US-10-066-521-6 (1-1344) x US-10-781-294-19 (1-2046)

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QY      8 ThrPheSerSerTy-----GlyLeuGlnTrpCySLeuTyGlu 20
      |||||
DB      82 ACATTCCTTGTGTAACCCGGCTCCCATGTGAAAATGGGGTCACTGTACATGAAGAAC 141
      |||||
QY      21 LeuAspLySGluPheGlnThrPheLySGluLeuLeuLySLeuSerSerGluSer 40
      ::::
DB      142 GTGAGCCATAGAGAGCTACACAGCTTCAAGCAGCTCTTCTGACTGACGTCACT--ACT 198
      |||||
QY      41 ThrThrCysSerLLeuProGlnPheGlnLLeuLysLLeuValLLeuValLLeu 60
      |||||
DB      199 GGCACATGCCCATCCTGGGACACAGTGCAGACACACCTGGGACAGGTGTTCCAT 258
      |||||
QY      61 LeuLeuHisGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 80
      |||||
DB      259 CTCCTGTATGAGCGCTTCCCTGACGACGCGCTTGGATGTGACTTGCACATCTTTGCC 318
      |||||
QY      81 AsnMetAsnLeuArgThrLeuSerGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 100
      ::::
DB      319 ATTATGAACTGTGATAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 378
      |||||
QY      101 AlaMetGluGlnGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 120
      ::::
DB      379 ACCCTGGACACAGGACTTGAATGTGGAGAAACACAG-----417
      |||||
QY      121 MetGluGlnGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 140
      |||||
DB      418 -----GTGAATCTGGAGGAAGGAAGGAATCTGGTAAATA 450
      |||||
QY      141 TrpAspTyTyTySerHisValMetThrThrPheHisGluGluGluGluGluGluGluGlu 160
      |||||
DB      451 CGGCGGATTAATGCAATGTGATGCAAAAGTTTTCCTCCCATATGGACATT-----501
      |||||
QY      161 PheGluAsnThrAlaAlaAspTrpProGluMetGlnThr-----LeuAlaGlyAla 177
      |||||
DB      502 -----ACGACTTGGCTGGAACACAGAGGACTTCTTCTACCAAGGTGTA 546
      |||||
QY      178 PheAspSerAspArgTrp-----GlyPheArg 186
      ::::
DB      547 CACAGGACGAGGAGTACTTACCATGTCTGTCTGTCTGCCCAAAAGACCCAGGTAAGACAG 606
  
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QY      187 ProArgThrValValLeuHisGlyTySerGlyLLeuTyLysSerAlaLeuAlaArg 206
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DB      607 CCCAAGACCTGGCCCATACAGGAGAGCTCCCTGGATGGGAAAACATCTCGGCCAAAG 666
      |||||
QY      207 LLeuValLeuCySLeuPheGlnGluGluGluGluGluGluGluGluGluGluGlu 226
      ::::
DB      667 GTGATGTTTGAAGGGGCAAAAACAGTTCTACGCCCAAGGCGCTGGTGTCTTCTAC 726
      |||||
QY      227 LeuProValArgLLeuMetGlnArgTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 246
      |||||
DB      727 TTCATATGCCAAGAGGGAACCAAGACACAGACAGAGCTTCTCCAGCTGATTAAGCAA 786
      |||||
QY      247 GluTrpProAspSerGlnAlaProValThrGluLLeuSerArgProGluArgLeu 266
      ::::
DB      787 AAGTGGCTGATCTCAGAGACCTCGTGTCAAAATATGTCCAAACCCAGCAACTCTTG 846
      |||||
QY      267 PheLLeuLeuAspGlyPheAspAspLeuGlySerValLeuAsnAspThrTyS--Leu 285
      ::::
DB      847 CTGCTCTGTGATGGCTTGAAGAGCTCACATCACTTACCTTGAACAGACTGAGAGACTG 906
      |||||
QY      286 CyLeuAspTrpAlaGluTyGlnProProPheThrLeuLLeuLysSerLeuArgTyS 305
      ::::
DB      907 AGTGAAGACTGAGGCGCAAGAAATGCTGGGTCTGTCTTACTGACAGATTGCTGAGAAA 966
      |||||
QY      306 ValLeuLeuProGluSerPheLeuLLeuValThrValArgAspValGluTyTyTyTy 325
      ::::
DB      967 ACGATGCTTCAGAGGCGCAGCTATGATCATGATTAAGATTACCTTGGACACATGC 1026
      |||||
QY      326 LysSerGluValValSerProArgTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 345
      ::::
DB      1027 AAGCCCTTGTGAAATGCTCCCTCTGTGAACTTCCGGGGTTTAAATGATGAGAAA 1086
      |||||
QY      346 LLeuHisLeuLeuLeuGluArgGlyLLeuGluLLeuHisGlnThrGlnGluArgAla 365
      |||||
DB      1087 ATCAAGATTTTCCAGATGTATTTTGGACACACAGAGGAGGAACCAAGCTTGAATTC 1146
      |||||
QY      366 LLeuMetAsnAsnArgLeuLeuLeuAspGlnCysGlnValProAlaValGlySerLeu 385
      |||||
DB      1147 GCCATGAAAACACCATCTCTTCTCCATGTGCGGGTCCCTGTGTGTCTGTGATGTGC 1206
      |||||
QY      386 CyValAlaLLeuGlnLeuGlnAspValValGlyLysSerValAlaProPheAsnGlnThr 405
      ::::
DB      1207 TGCCTGTGTGAAACAGCAATGGAAGAGAAAC-----AATCTCACA 1251
      |||||
QY      406 LeuThrGlyLeuHisAlaAlaPheValPheHisGlnLeuThrProArgGlyValAlaArg 425
      ::::
DB      1252 CAGTCAATGTCCAAATGCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1311
      |||||
QY      426 ArgCySLeuAsnLeuGluArgVal-----ValLeuLysArgPheCyValArgMet 442
      |||||
DB      1312 AGAGCTGAGAACTTTTCCAGAAAGATCCCAAGACACAACTGGAAGGTGTGTCACTTG 1371
      |||||
QY      443 AlaValGluGluValTrpAsnArgTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 462
      ::::
DB      1372 GCGGCAACAGCAAGTGGCAAGGAAATGGGTGTAGTAAAGAAATCTTGAAGAAAGCC 1431
      |||||
QY      463 GlyLeuGlyLysSerGluLeuArgAlaLeuPheHisMetAsnLLeuLeuProAspSer 482
      |||||
DB      1432 AAGCTGATCAAGACGGAGAGTCAACCGCTTCTGGCATGAGTATCTTCTGGAGAAATGCA 1491
      |||||
QY      483 HisCySLeuGluTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 502
      ::::
DB      1492 GGTGAGGAAGACACATGTGTCTTACCGCTGTGACTTTCAGGAATTTTGTGGCGCTTG 1551
      |||||
QY      503 TyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 519
      ::::
DB      1552 TTTTATGTCTGTGTCTTCCACAAAGACTCAAAATTTTCAATGTGTGAGCCACGTAAAT 1611
      |||||
QY      520 ValGluTyThrTyTyTySerMetGluLeuTyGlnAlaGlyPheHisLLeuSerLeu 539
      ::::
DB      1612 ATCCAGGCGCTGATAGAGAT-----CCAGAGGAAGCAAAAGCTATCTCTCT 1659
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QY      540 TrpMetLysArgPheLeuPheGlyLeuValSerGluAspValArgArgProLeuGluVal 559
  
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Db 1660 CACATGGAGCTTTCTTATTCGGTTTCTGAACAGAGCCCTGCGCTGGCGGTGAACAG 1719

Qy 560 LeuLeuGlyCysProValProLeuGlyValYlyLeuLeuHisTrpValSerLeu 579

Db 1720 TCATTCGAATCAAGAGTGTCTTTCGGTAATAAGAGAACTGCTGAAGTCAATACCTCTG 1779

Qy 580 LeuGlyGlnGlnProAsnAlaThrThrProGlyAspThrLeu---AspAlaPheHisCys 598

Db 1780 TTG---CATTAATGTAGACCACTTCTCCGGAGTGGGGTCCCGCACTTATTCACGT 1836

Qy 599 LeuPheGlnThrGlnAspLeuGlyGluPheValArgLeuAlaLeuAsnSerPheGlnGluVal 618

Db 1837 CTCGATGAATATCCGGAGAGAACCTTTGTATGCCAGCCCTTAATGATATCATTAAGTT 1896

Qy 619 TrpLeuProIleAsnGlnAsnLeuAspLeuIleAlaSerSerPheCysLeuGlnHisCys 638

Db 1897 GCTTGAAGATTTGGCAACAAAGAAAGTTCAAGTCTGCTTTTGGCTGAAAGCGGTGT 1956

Qy 639 ProTyrLeuArgLysIleArgValAspVal 648

Db 1957 CAATATTTCATGAGTGAAGTGAACCTGACCGTC 1986

RESULT 15

US-08-910-731-3

Sequence 3, Application US/08910731

Patent No. 5932440

GENERAL INFORMATION:

APPLICANT: CHATTERJEE, DEB K.

APPLICANT: SHANILVA, HARINI

TITLE OF INVENTION: Mammalian Ribonuclease Inhibitors and Use Thereof

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., N.W., SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,731

FILING DATE: (Herewith)

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/795,395

FILING DATE: 04-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/794,546

FILING DATE: 03-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/024,057

FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: ESMOND, ROBERT W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0942.3440003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1374 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1368

US-08-910-731-3

Alignment Scores:

Pred. No.: 2,54e-53

Score: 630.50

Percent Similarity: 51.38%

Best Local Similarity: 34.63%

Query Match: 8.91%

DB: 2 Gaps: 3

US-10-066-521-6 (1-1344) x US-08-910-731-3 (1-1374)

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Db 39 CCGGAGCAAGAGCTCTTCCCTGATCCAAATACCAAG-TGGTC-AGCGTGAATAC 96

Qy 671 LysThrLeuIleGlnGlnGlnTrpGluAspPheCysSerMetLeuGlyThrHisProHis 690

Db 97 TGTGGCTCTCAAGAGTGGTGAAGATCAAGATCAGGTGAGGATCCAGGCCAACCCTGCC 156

Qy 691 LeuArgGlnLeuAspLeuGlySerSerIleLeuThrGlnArgAlaMetLysThrLeuCys 710

Db 157 CTGACAGAGCTCAGGCTTACGACCAATGACTGGGTGATGCTGTGGTGTGCTGCTC 216

Qy 711 AlaLysLeuArgHisProThrCysLysIleGlnThrLysMetPheArgAsnAlaGlnIle 730

Db 217 CAGGCTCTGCAAGATCCACTTGTATGATCCAGAGCTGAGCCTTCAAGATCGACGCTTG 276

Qy 731 Thr---ProGlyValGlnHisLeuTrpArgIleValMetAlaAsnArgAsnLeuArgSer 749

Db 277 ACGGAAGCTGGGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGA 336

Qy 750 LeuAsnLeuGlyGlyThrHisLeuLysGlnGluAspValArgMetAlaCysGlnAlaLeu 769

Db 337 CTACATCTCAATGACCAACCTCTGGGGATGAGAGCTGAGCTGCTGTGAAGAGACTC 396

Qy 770 LysHisProLysCysLeuLeuGlnSerLeuArgLeuAspCysGlyLeuThrHisAla 789

Db 397 CGGAGCCCCAGAGCTCCCTTGAAGAGCTTCAAGTGAATACTGTAACTCACTCACTACC 456

Qy 790 CysTyrLeuLysIleSerGlnIleLeuThrThrSerProSerLeuLysSerLeuSerLeu 809

Db 457 AGCTCGAGCCCTGGCTCAGTCTCAGGAGGAACTGACTTTAAAGAGCTAGATATTT 516

Qy 810 AlaGlyAsnLysValThrAspGlnGlyValMetProLysSerAspAlaLeuArgValSer 829

Db 517 AGCAACAATGACTTCATGAGGCTGTGTATCCACACTCTGTGCAGGGCCCTGAAGATTC 576

Qy 830 GlnCysAlaLeuGlnLysLeuIleLeuGlnAspCysGlyIleThrAlaThrGlyCysGln 849

Db 577 GCCTGTCAACTGAGATCACTCAAACTGGAAGACTGTGTATCAATCAAGCCAACTGCAAG 636

Qy 850 SerLeuAlaSerAlaLeuValSerAsnArgSerLeuThrHisLeuCysLeuSerAsnAsn 869

Db 637 GATCTGTGTGATGTTGTGGCTTCAAGGCTCCTCAAGGCTCAGAAAGTGAAGTGGAGAAC 696

Qy 870 SerLeuGlyAsnGlnGlyValAsnLeuLeuCysValArgSerMetArgLeuProHisCysSer 889

Db 697 AAGCTGGGCAACACAGGATTCAGACACTGTCTCAGGACTGTCTTCCAGCTGCAGG 756

Qy 890 LeuGlnArgLysMetLeuAsnGlnCysHisLeuAspThrAlaGlyCysGlyPheLeuAla 909

Db 757 CTGAGGACTCTGTGGCTTGGAGACTGTATGATGATGATGATGATGATGATGATGATG 816

Qy 910 LeuAlaLeuMetGlyAsnSerTrpLeuThrHisLeuSerSerMetAsnProValGlu 929

Db 817 CGTGTCTCAGAGCCAGAGAGCTGAAAGAACTCAAGCTTGTGGCTGAGCTGAGAG 876

Qy 930 AspAsnGlyValLysLeuLeuCysGlnValMetArgGlnProSerCysHisLeuGlnAsp 949

Db 877 GATGAGGGTCCCAACTGCTGTGTGAGAGCTGTGAAGCTGTGGCTGTGCTGAGCTGAGTCA 936

